Fratoria BV
Westewagenstraat 60
3011AT Rotterdam
The Netherlands
Email: info@fratoria.com
Web: www.fratoria.com

Fratoria DICOM RT Studio

User Manual

Release 1.9.0

June 2011

CE 1639

Contents

1 What's new 5

1.1 Release 1.9 5

2 Installation Instructions 6

3 Minimum Hardware Requirements 6

4 Loading Data 6

4.1 Loading from a folder 6

4.2 Loading from a PACS 7

4.3 Loading Image 9

4.4 Loading active MOSAIQ patient 9

4.5 Loading 4D data 10

4.6 Object Linking 10

4.7 Importing and exporting application configuration 11

4.8 Using command line arguments 11

5 Projects 12

5.1 Saving projects 12

5.2 Loading projects 12

6 Application Overview 13

6.1 Layout 13

6.2 Toolbar 13

6.3 Navigation and interaction 14

6.4 Windows 15

7 Image orientation 15

8 ROIs 15

8.1 Visible ROIs 15

8.2 Contour selection 16

8.3 Contour line width and color 17

9 POIs 17

10 Beams 18

10.1 IMRT Plans 19

10.2 Dynamic Arc Plans 19

10.2.1 Beam Intensity Diagram 20

10.2.2 Live Beams-Eye-View 21

11 Dose 21
11.1 Dose lines and colorwash 22
11.2 Visible Dose Values 22
11.3 Dose Volume Histogram (DVH) 23
11.4 Dose Accumulation and Dose Difference 24
11.5 Dose Objects 25
12 DRR 25
13 Distance measurement 26
14 Position Tracking 27
15 Cropping 27
16 Image Window / Level 28
17 Magnifier 29
18 Reporting Tool 30
19 3D viewing 32
19.1 Volume and Surface rendering 32
19.2 Skin with collimator outlining 32
19.3 3D settings 33
19.4 Shade 35
19.5 3D slice positions 35
20 PET-CT 35
20.1 PET options 36
21 Viewing registered images 37
22 Plan comparison 38
23 4D 39

Device description

Fratoria DICOM RT Studio is a software toolbox for advanced radiotherapy viewing, analysis and contouring based on DICOM and DICOM RT. It allows the user to read all relevant radiotherapy data, including images, plans, dose, ROIs/POIs and RT images, view this data interactively in 2D/3D/4D and evaluate plans. Optionally, the user may do contouring with the contouring plug-in and save the result as DICOM RT structure for use by other systems in the delivery of treatment to a patient.
The contouring module is described in the user manual for contouring.

The system runs as a stand-alone application on Microsoft Windows platform.

Intended use

The software is to be used by radiation oncology professionals for:

- review and evaluation of radiotherapy plans and all related imaging data;
- contouring for the purposes of creating patient treatment plans in radiotherapy Treatment Planning Systems with the contouring data generated by the contouring module for Fratoria DICOM RT Studio. This is applicable to contouring module only.

Intended audience

This manual is written for radiation oncology professionals and for Fratoria software (service) engineers. You should make sure that you have thoroughly read and completely understand the manuals and release notes that are delivered with the software.

If you suspect that the system does not operate according to this manual, discontinue its use and contact Fratoria customer support by email via info@fratoria.com.

CE Marking

Fratoria DICOM RT Studio is CE market to the Medical Device Directive 93/42/EEC.

CE 1639

Disclaimer

All rights reserved ©2011: Fratoria BV

All the information in this document is intellectual property of Fratoria BV.
The content of this document may not be reproduced or published without written permission from Fratoria BV.

1 What's new

1.1 Release 1.9

1. Visualization of merged CT/MR images with projected RT objects.
2. Side by side comparison of two plans on the same set of CT images
3. Improved DVH module with the ability to compare calculated DVHs of two plans and DVH statistics
4. Project files allowing to save study location with viewing presets.
5. Result of Dose Difference calculation shows which of two plans is better using positive and negative dose.
6. Improved visualization of Beam Intensity Diagram for dynamic arc plans
7. Labels for identification of dose objects (e.g. total dose, dose per beam) in Dose Objects overview
8. "Study date" added to the PACS search results window

2 Installation Instructions

In order to install Fratoria DICOM RT Studio you first have to obtain your hardware ID. Therefore, run FratoriaGetIDS.exe and copy the generated unique hardware ID. When contacting Fratoria, you will be asked for this ID to generate a serial number for your license.

To install the application, just run the .msi installation file (you might have to unzip it first) and follow the instructions on the screen. At the end of the installation you will be asked to enter your serial number.

3 Minimum Hardware Requirements

Two versions of the application are available - 32-bit and 64-bit.

The 32-bit version will run on any Windows based PC/laptop with Windows XP, Windows Vista or Windows 7, at least 1GB of RAM, 1024 x 768 screen resolution and a reasonably modern mainstream GPU . The 64-bit version requires a 64-bit Windows platform.

4 Loading Data

You can load a dataset either by loading it from a local folder or from a PACS server. You can also load separate images and 4D datasets from a local folder. The process of data loading can be monitored in the console window (see Figure 1.)

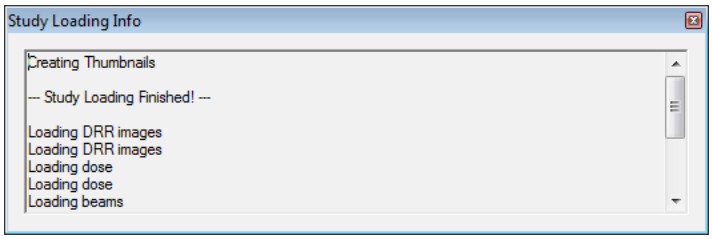

Figure 1 Study Loading Info

You can load more than one dataset, if your machine has enough memory, and switch between them using drop-down menu with patient names (see Figure 5).

4.1 Loading from a folder

In order to load a dataset from a local folder you have to select from the main menu File->Load Local Dataset and then select a folder from a tree structure.

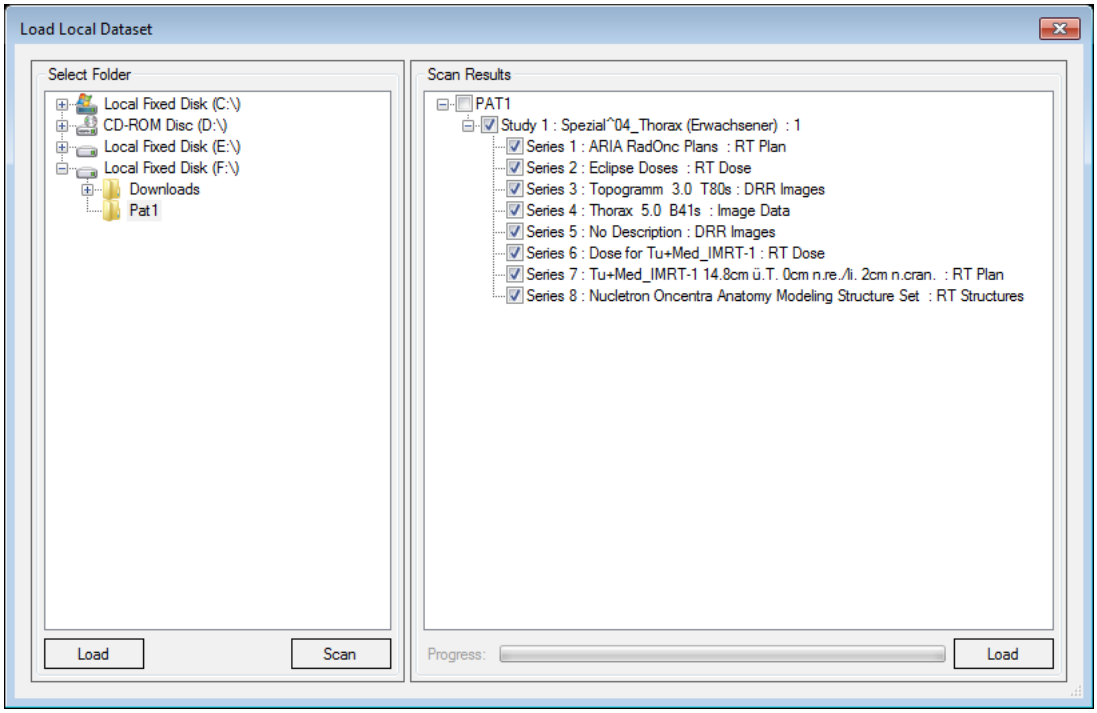
Load Local Dataset
Select Folder
Local Fixed Disk (C:\)
CD-ROM Disc (D:\)
Local Fixed Disk (E:\)
Local Fixed Disk (F:\)
Downloads
Pat1
Load
Scan
Scan Results
PAT1
Study 1 : Spezial^04_Thorax (Erwachsener) : 1
Series 1 : ARIA RadOnc Plans : RT Plan
Series 2 : Eclipse Doses : RT Dose
Series 3 : Topogramm 3.0 T80s : DRR Images
Series 4 : Thorax 5.0 B41s : Image Data
Series 5 : No Description : DRR Images
Series 6 : Dose for Tu+Med_IMRT-1 : RT Dose
Series 7 : Tu+Med_IMRT-1 14.8cm ü.T. 0cm n.re./li. 2cm n.cran. : RT Plan
Series 8 : Nucletron Oncentra Anatomy Modeling Structure Set : RT Structures
Progress:
Load

Figure 2 Load Local Dataset

There are two possibilities to load a dataset:

1) You can either select a directory and click on "Load" button in the left panel.
   The application will load all the dicom data from the subfolders. You can have your scans, RT images, RT structures, dose and plan files in different subfolders. The application will combine the data that belong to the same plan. You may load several plans at a time if they are stored in subfolders by selecting a higher level folder. The application will ignore all non-dicom data that might be present in the folder(s).
2) You can select a directory from the left panel and click on "Scan" button.
   The application will analyze the directory structure and present a tree view in the right panel, as shown on Figure 2. The tree view has the following structure: Patient name -> Study#: Study description: Study-id -> Series#: Series description: Series type. You can select one or more studies, and one or more series.
   Note: If you select an RT dose object that does not have a corresponding plan or you do not select the corresponding plan, the application will create an empty plan automatically during the data loading.

4.2 Loading from a PACS

To load a study from a PACS server, select File->Load Remote Dataset. The window shown on Figure 3 will appear.

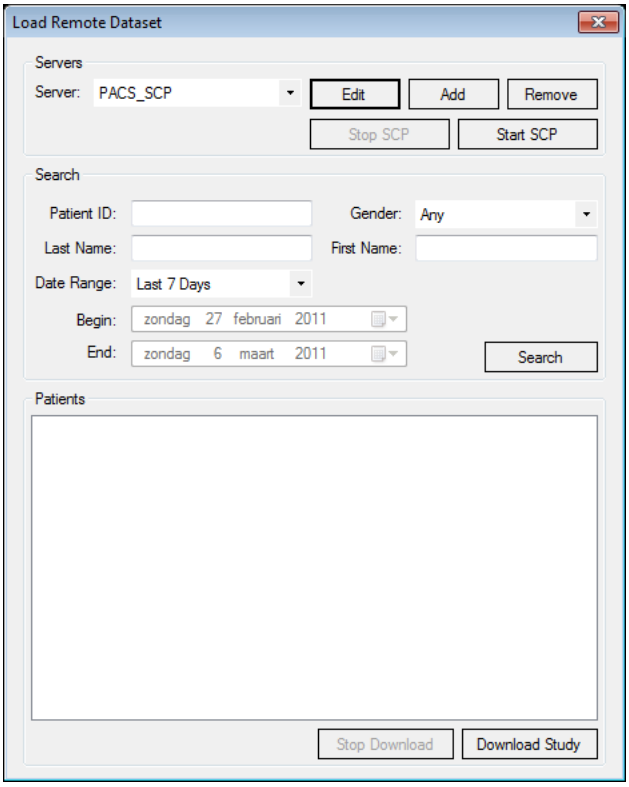

Figure 3 Load Remote Dataset

If you have not connected to your PACS server yet or do not have the right server on the list, click on Add Server button. The following window will appear:

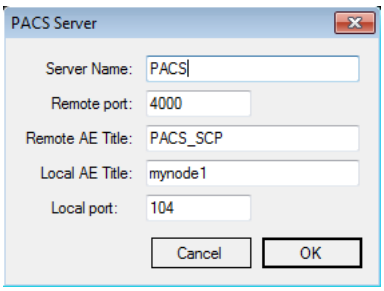

Figure 4 Add/Edit PACS Server

Here you have to provide the name or ip-address of the PACS server, Remote port, remote and local AE titles and Local port. Your Local AE Title must match with the AE title added as a dicom node to the PACS server. Note that you should properly add your application node as a dicom node to the PACS server. The default Local port is 104, but if you have, for example, several DICOM listeners that cause a conflict, you can adjust it.

After you have selected a PACS server, you can download the data either 1) by searching for a study in the PACS and sending it to the DICOM RT Studio, or 2) by using the Search feature in the DICOM RT Studio to select and download the study.

For 1) you have to click on Start SCP button and then search for a study in your PACS and send it to this dicom node.

For 2) you can define your search criteria and click on the Search button (see Figure 3). If data are available, a tree with patient names will be presented. Every patient contains a list of studies. A study contains a list of modalities. You can select patient, one or more studies, or just several modalities belonging to a study and click on the Download Study button. The download process can be monitored as shown on Figure 1.

4.3 Loading Image

To load an image, go to File->Load Image and select a file. The application will open it in the Image Viewer.

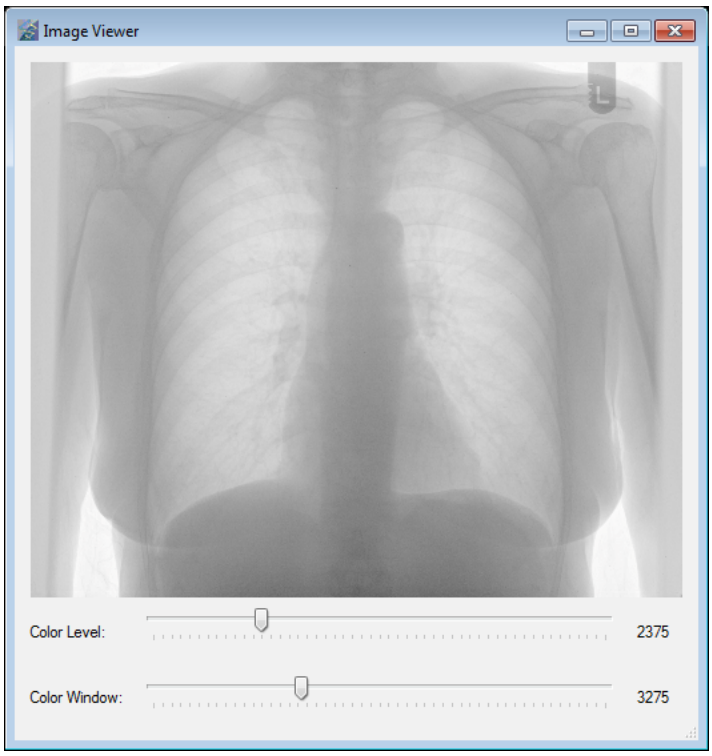

Figure 5 Image Viewer

In the Image Viewer you can:

- Adjust Level and Window settings using the sliders,
- Rotate image with the mouse by pressing Ctrl + left mouse button,
- Move image with the mouse by pressing Shift + left mouse button,
- Zoom in and out by pressing right mouse button and moving the mouse cursor up and down,
- Change window size.

4.4 Loading active MOSAIQ patient

The application can be connected to MOSAIQ from Elekta/Impac to load the active patient-id and obtain all plan data available for that patient from a PACS.

IMPORTANT! In order to connect to MOSAIQ, the parameter *WorkstationID* must be specified in impac.ini file on every workstation running MOSAIQ and where connectivity with Fratoria DICOM RT Studio should be implemented.

When opening a patient in MOSAIQ, it will create a *patid* file that will contain the id of the active patient. The *patid* file will have an extension corresponding to your *WorkstationID*. For example, if you put *WorkstationID=001* in impac.ini, MOSAIQ will generate *patid.001*.

Go to File->Load Active MOSAIQ Patient and you will be presented with a window where you should select the location of the *patid* file. Once selected, the application will remember the location of this file and will not ask you next time when to try to load active MOSAIQ patient.

After confirming the patient-id, the application will open the Load Remote Dataset form, as shown on Figure 3, fill in the patient-id and send the query to the PACS server specified in the drop-down menu. You can then select and download dicom (rt) data of this patient from the PACS.

4.5 Loading 4D data

To load a 4D dataset, go to File->Load 4D Dataset. The application will present the data in 3D as a volume looping through the timeframes. The timeframe control (see Figure 7) will become enabled, so you can browse not only through the slices, but also through individual frames in 2D.

4.6 Object Linking

After the data has been loaded into application, you can verify the references between the objects in the dataset and create or remove links if necessary for correct visualization.

In some scenarios, for example, when the scans have been exported separately from the plan, they are stored most probably under different study uid's and the reference will be missing. Another example could be several dose objects, such as prescribed dose and portal dosimetry dose that need to be visualized on a set of CT scans and therefore should be linked to a plan.

To view the structure of the loaded dataset, go to the menu File->Object Linking. A screen, like the one show on Figure 6 will be presented.

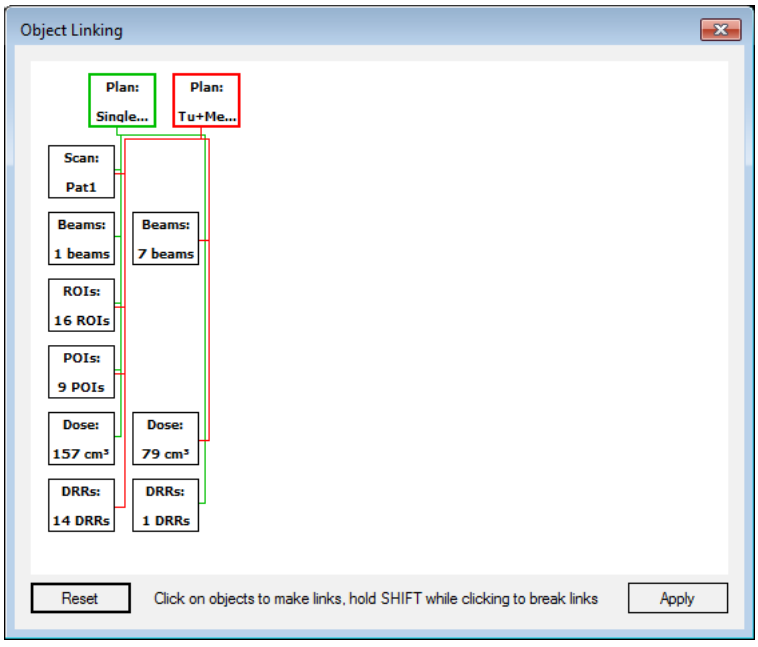

Figure 6 Links between RT objects

When hovering with the mouse above the objects a pop-up window will be shown containing information about the object. When hovering above a Plan object, the links to all objects with the reference to the plan will be highlighted.

To enter editing mode, click on Plan object. This will highlight the links to the connected objects. Click on the objects to make links. Hold SHIFT while clicking to break links. Click on Apply button to make the changes visible in the application. The Reset button brings the object linking diagram to the state before the last change has been applied.

IMPORTANT! Only one dose object can be connected to a plan. Orphan dose is not allowed by the DICOM standard. If you have an orphan dose in the dataset that has no reference to the plan, or the plan object is missing, the application will create an empty default plan and connect that dose to the newly created plan automatically.

4.7 Importing and exporting application configuration

All user settings in the application are kept in the xml configuration file. It contains:

- data from Figure 4 entered to establish connection with PACS system(s);
- user defined profiles for image window/level settings;
- user defined schemes for visible dose values;
- user preference for calculation of coronal and sagittal contours (manual vs. automatic);
- the last selected folder for loading from the hard disc;
- presets for volume rendering.

You can export these settings to an xml file and import, for example in the application on another workstation, by going to File->Export Configuration and File->Import Configuration.

4.8 Using command line arguments

Using the following command line arguments the application can be launched and load automatically the data specified in the command line, either from a local directory, or from a PACS server:

-L (Load local dataset)
-R (Load remote dataset)
-P “path for the local dataset”
-S “PACS server ip-address or name”
-laet “Local AET”
-raet “Remote AET”
-port "number" (remote port on PACS)
-patid “PATIENT ID”
-suid “Study UID”
-seruid “Serie UID”

Options -L and -R are mutually exclusive.

If only patid is provided, all studies for this patient will be loaded, either from a folder on the hard disc or from a pacs server.

Example for loading a local dataset:

“Fratoria Dicom RT Viewer.exe –L –P C:\DicomData\RTDataset –suid 1.2.840.113745.101000.1008000.38220.6657.6448998”

Example for loading a remote dataset:

“Fratoria Dicom RT Viewer.exe –R –S PACS-NAME –laet fratoria1 –raet PACS_REMOTE_AE –port 4006 –suid 1.2.840.113745.101000.1008000.38220.6657.6448998”

To load multiple datasets, the –L or –R options can be used several times, for example:

“Fratoria Dicom RT Viewer.exe –R –S PACS-NAME –laet fratoria1 –raet PACS_REMOTE_AE –port 4006 –suid 1.2.840.113745.101000.1008000.38220.6657.6448998 –R –S PACS-NAME –laet fratoria1 –raet PACS_REMOTE_AE –port 4006 –suid 1.2.840.113745.101000.1008000.38220.6657.6448999”

5 Projects

5.1 Saving projects

Application state for a particular dataset can be saved as a project file. It allows you to define the layout with visible dose, beams, ROIs, etc. and save it, together with the location of the loaded dataset, in an XML project file for fast retrieval.

To save a project file, go to the menu File->Save Project and provide a name for the XML files. The following parameters will be saved:

- Location of the current dataset (either on hard disc or in PACS)
- Active plan
- Visible ROIs
- Visible beams with control points
- Display of dose lines and colorwash
- Selected dose color scheme
- Display of absolute or normalized dose, including POI for normalization
- All and visible dose values for selected color scheme"DoseValues"
- PET if selected, together with PET color scheme, window and level settings, and the X,Y,Z shift
- Overlay image if selected, including width and height of checks for check board display, overlay opacity an color.
- For the 3D rendering window: Mode, Show ROIs, Show POIs, Show Beams, Show Dose
- Window and Level setting for 2D image display
- The number of the displayed transversal, coronal and sagittal slice
- Whether or not to display Live Beams-Eye-View

Note, that if you saved a project file with a specific color scheme and intend to open it later on another computer and, you need to have this color scheme on the target computer.

5.2 Loading projects

To load a project, go to the menu File->Load Project and select an XML project file. The dataset will be automatically loaded and the application will be brought to a state according to the saved presets.

6 Application Overview

6.1 Layout

After you have loaded a data set, the application would look like the one presented on Figure 7.

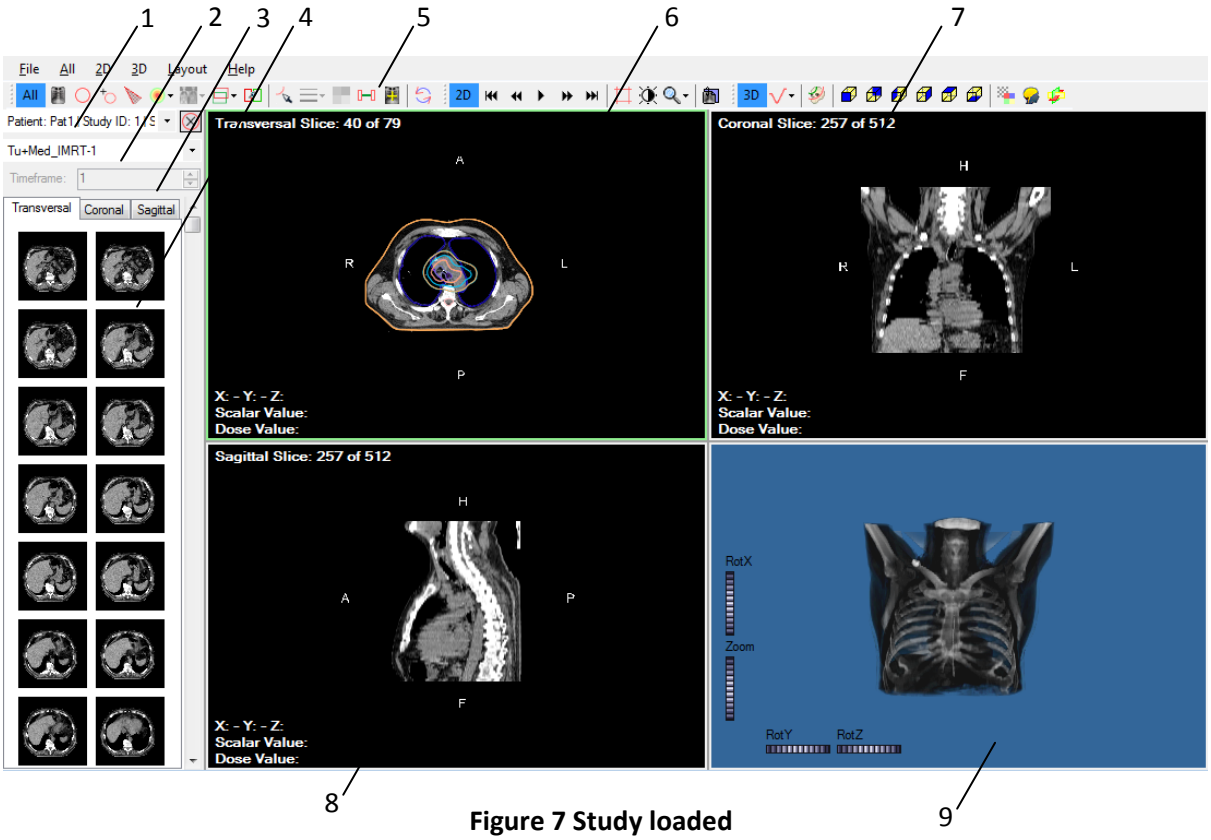

Figure 7 Study loaded

The layout consists of the following components:

1 – Drop-down menu with patients names from the loaded studies.
2 – Drop-down menu with plans associated with the active study.
3 – Timeframe selector to browse through frames in 4D datasets.
4 – Thumbnail panel containing Transversal, Coronal and Sagittal thumbnails.
5 – Toolbar with shortcuts to the main application features.
6 – Transversal view.
7 – Coronal view.
8 – Sagittal view.
9 – Interactive 3D viewer.

When you click inside a viewing window, it becomes active. By selecting items from the Layout menu, you can make any of the viewing windows appear larger. Alternatively, you can drag the vertical and horizontal window separators to define your own layout.

6.2 Toolbar

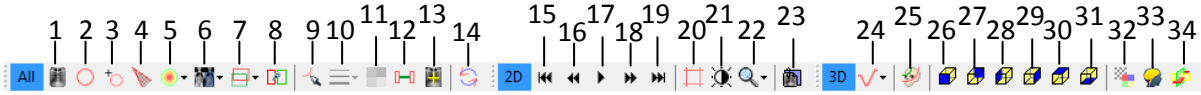

Figure 8 Toolbar

The toolbar is split into 3 sections: Generic, 2D en 3D tools. All functions can also be called from the main menu.

Generic tools 1-14:

1: DRR Viewer – view stored DRR's and/or generate DRR's with collimator outlines.
2: ROIs – select visible ROI's
3: POI's – select visible POI's
4: Beams – select visible Beams and beam control points.
5: Dose – tools to show dose lines and colorwash, DVH and define visible dose values
6: PET – select PET scans to project on CT and set preferences with PET Options tool
7: Overlay - view registered images
8: Compare plans - view two plans side by side
9: Contour selector – select contours in a ROI
10: Contour line width – change line with of selected contour/ROI
11: Contour line color – change color of selected contour/ROI
12: Measuring tool – measure distance between 2 points on a slice
13: Position Tracking - track position of a point selected in a 2D view in other views
14: Reset – reset all properties for all viewers

2D tools 15-23:

15-19: Slice scrolling tools: First, Previous, Loop/Pause, Next, Last
20: Cropping – crop volume using 2D manipulators
21: Image Window/Level – adjust Window/Level settings
22: Magnifier – zoom in/out on image details
23: Reporting tool: generate reports containing selected images in a grid layout

3D tools 24-34:

24: Visible in 3D – define the type of rendering - volume, surface, or PET-CT - or Live Beams Eye View and the items to be made visible in 3D (POIs, ROIs, beams, dose)
25: Surface Rendering Options: define the type of surface rendering (skin, bone, etc.), including projection of the collimator outlining on the skin
26-31: 3D orientation tools: Front, Back, Right, Left, Top, Bottom
32: 3D Settings, including Opacity, Color mapping, Presets, and 4D options
33: Shade: shade for volume rendering
34: 3D Slice Positions – display positions of 2D slices as planes in 3D

6.3 Navigation and interaction

To browse through slices in 2D, you can click on the thumbnails, use keyboard arrows, mouse scroll wheel or navigation buttons 15-19 on the toolbar.

Interaction in 2D includes:

- Rotating image with the mouse by pressing Ctrl + left mouse button;
- Moving image with the mouse by pressing Shift + left mouse button;
- Zooming in and out by pressing right mouse button and moving the mouse cursor up and down.

Interaction in 3D includes:

- Rotation using RotX, RotY, RotZ scroll wheels, or by pressing left mouse button and moving the mouse cursor. You can also rotate around Z axis by pressing Ctrl and left mouse button;
- Moving by pressing Shift and left mouse button;
- Zooming in and out by pressing right mouse button and moving the mouse cursor up and down.

6.4 Windows

Via the menu Layout you can select which of the 4 windows should get enlarged: Transversal, Coronal, Sagittal or 3D. Alternatively, you can select Tile Even for even size. By dragging the vertical and horizontal separators you can also change the size of the windows.

7 Image orientation

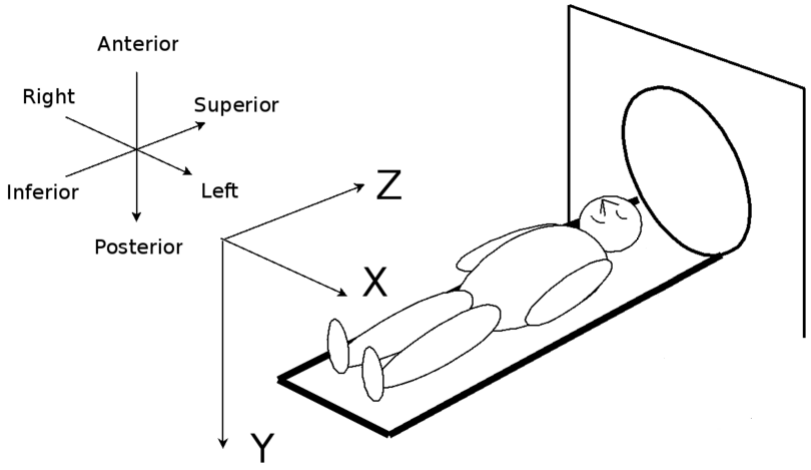

Figure 9 DICOM LPS Orientation

The direction of the axes is defined fully by the patient's orientation. The x-axis is increasing to the left hand side of the patient. The y-axis is increasing to the posterior side of the patient. The z-axis is increasing toward the head of the patient. The patient based coordinate system is a right handed system, i.e. the vector cross product of a unit vector along the positive x-axis and a unit vector along the positive y-axis is equal to a unit vector along the positive z-axis (see Figure 9).

8 ROIs

8.1 Visible ROIs

If the loaded study contains ROIs, they will be displayed automatically in transversal view.

You can make contours visible/invisible by first clicking on the Visible ROIs button on the toolbar (button 2 on Figure 8) or selecting All->Visible ROIs from the menu. It will bring up window shown on Figure 10 where you can check/uncheck ROIs.

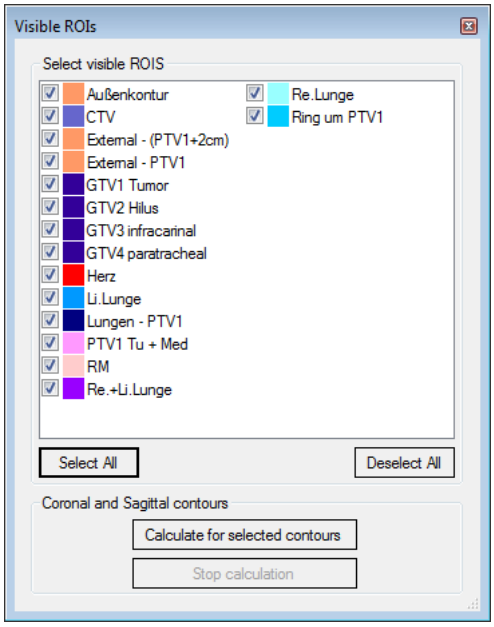

Figure 10 Visible ROI's

The application can also calculate coronal and sagittal ROIs based on transversal ones. This calculation runs on the background in a separate process and does not interfere with the normal operation. In the Visible ROIs window, select the ROIs and click "Calculate for selected contours" button. Individual contours of each ROI will appear on the coronal and sagittal slices as soon as they are calculated.

To show ROIs in 3D, go to 3D->Visible In 3D->Show ROIs, or click on the Visible In 3D button on the toolbar (button 24 on Figure 8) and select Show ROIs. ROIs are best viewed with semitransparent volume rendering, as shown on Figure 11.

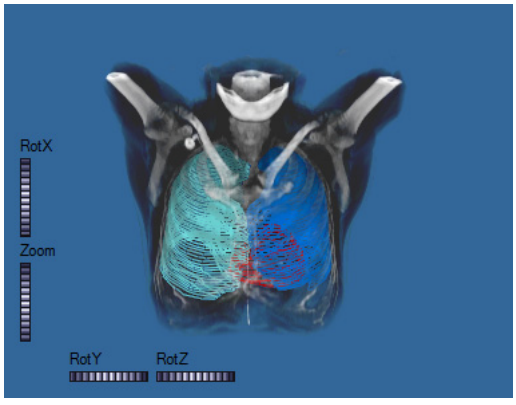

Figure 11 ROIs in 3D

8.2 Contour selection

To select a contour, first go to All->Select Contour or click on the Select Contour button on the toolbar (button 9 on Figure 8). Click then on or close to a contour that you would like to select. Contour name will appear at the bottom of the viewing window and an arrow will point on the selected contour.

Contours can be selected in transversal, coronal and sagittal views.

8.3 Contour line width and color

You can adjust the line width and color of the selected contour for better visibility in 2D and in particular in 3D view.

To change the line width, first select a contour as described in section “6.2 Contour selection”. Now go to All->Line Width, or click on the Line Width button on the toolbar (button 10 on Figure 8), and select line thickness 1 to 10. The application will ask you whether you want to apply this change to all contours in the ROI this contour belongs to. If you select “Yes”, all contours in this ROI will be given selected line thickness. If you choose “No”, the change will be applied just to the selected contour.

To change contour color, select a contour as described in section “6.2 Contour selection”. Now go to All->Line Color, or click on the Line Color button on the toolbar (button 11 on Figure 8), and select a color from the color pallet window that will appear. If you click “Ok” to confirm your color choice, the application will ask you whether you want to apply this change to all contours in the ROI this contour belongs to. If you select “Yes”, all contours in this ROI will be given the selected color. If you choose “No”, the change will be applied just to the selected contour.

To see the changes you applied to the selected contour or ROI in 3D, go to 3D->Visible In 3D->Show ROIs, or click on the Visible In 3D button on the toolbar (button 24 on Figure 8) and select Show ROIs. ROIs are best viewed with semitransparent volume rendering, as shown on Figure 12.

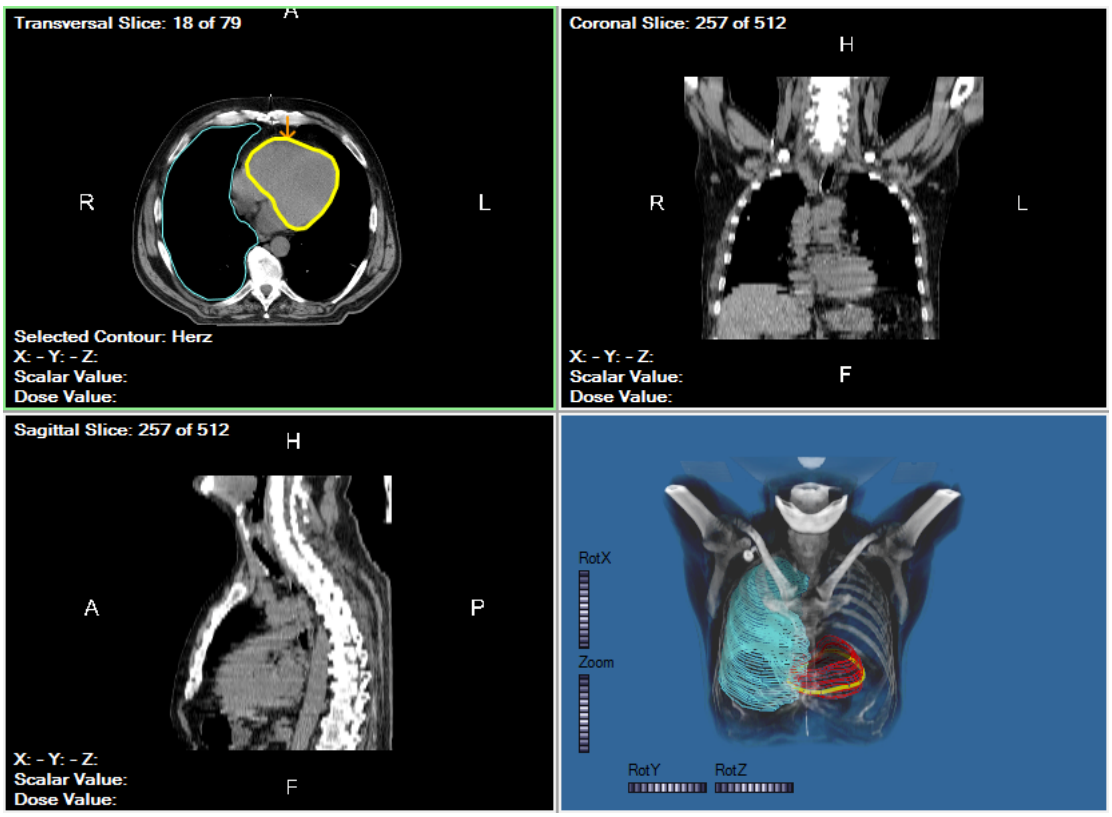

Figure 12 Selected contour

9 POIs

If the loaded study contains POIs, they will be displayed automatically in transversal, coronal and sagittal views as spheres with a cross on the slice coinciding with the center of POI.

You can make POIs visible/invisible by going to All->Visible POIs in the menu, or clicking on the Visible POIs button on the toolbar (button 3 on Figure 8). It will bring up window shown on Figure 13 where you can check/uncheck POIs.

To show POIs in 3D, go to 3D->Visible In 3D->Show POIs, or click on the Visible in 3D button on the toolbar (button 24 on Figure 8) and select Show POIs.

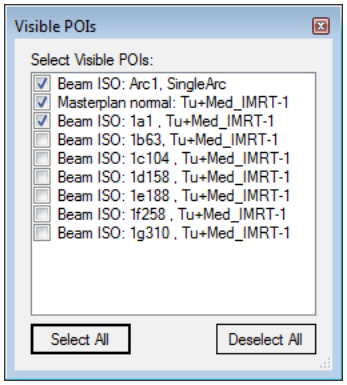

Figure 13 Visible POIs

10 Beams

To turn on beams, go to All->Visible Beams, or click on the Beams button on the toolbar (button 4 on Figure 8). Window as shown on Figure 14 will appear.

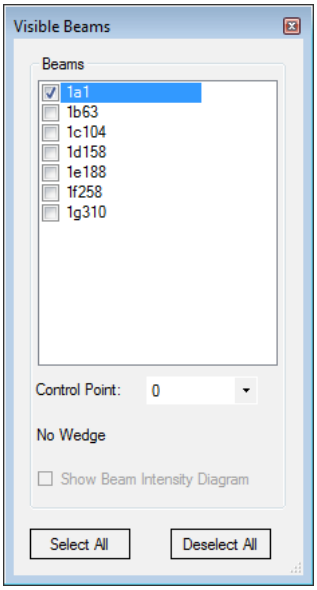

Figure 14 Visible Beams

To view beams in 3D, go to 3D->Visible In 3D->Show Beams, or click on the Visible In 3D button on the toolbar (button 24 on Figure 8) and select Show Beams.

10.1 IMRT Plans

IMRT plans have beams with more than one control point. When you click on a beam in Visible Beams window, Control Point drop-down box will become enabled if the beam has multiple control points. By clicking on the Control Point drop-down box and holding the arrow keys you can loop through the list of control points.

An example of IMRT plan is shown on Figure 15.

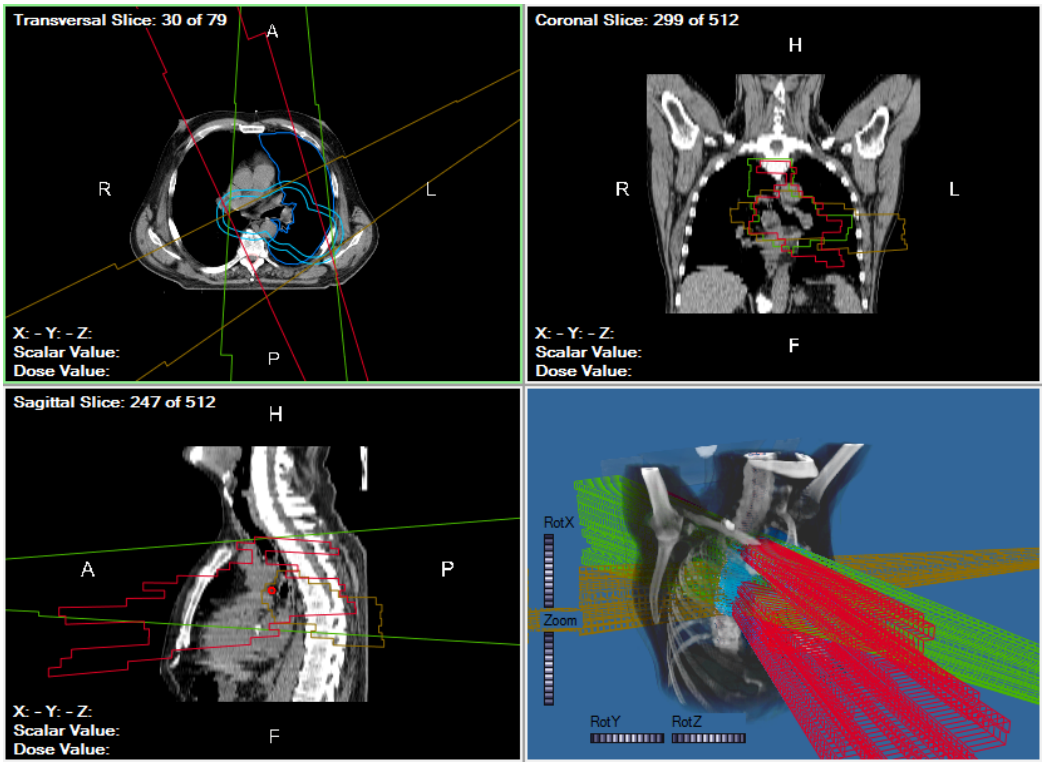

Figure 15 IMRT plan visualization

10.2 Dynamic Arc Plans

Visualizations of Elekta VMAT and Varian RapidArc plan are similar. An example of an RapidArc plan with Beam Intensity Diagram and Live Beams-Eye-View is shown on Figure 16.

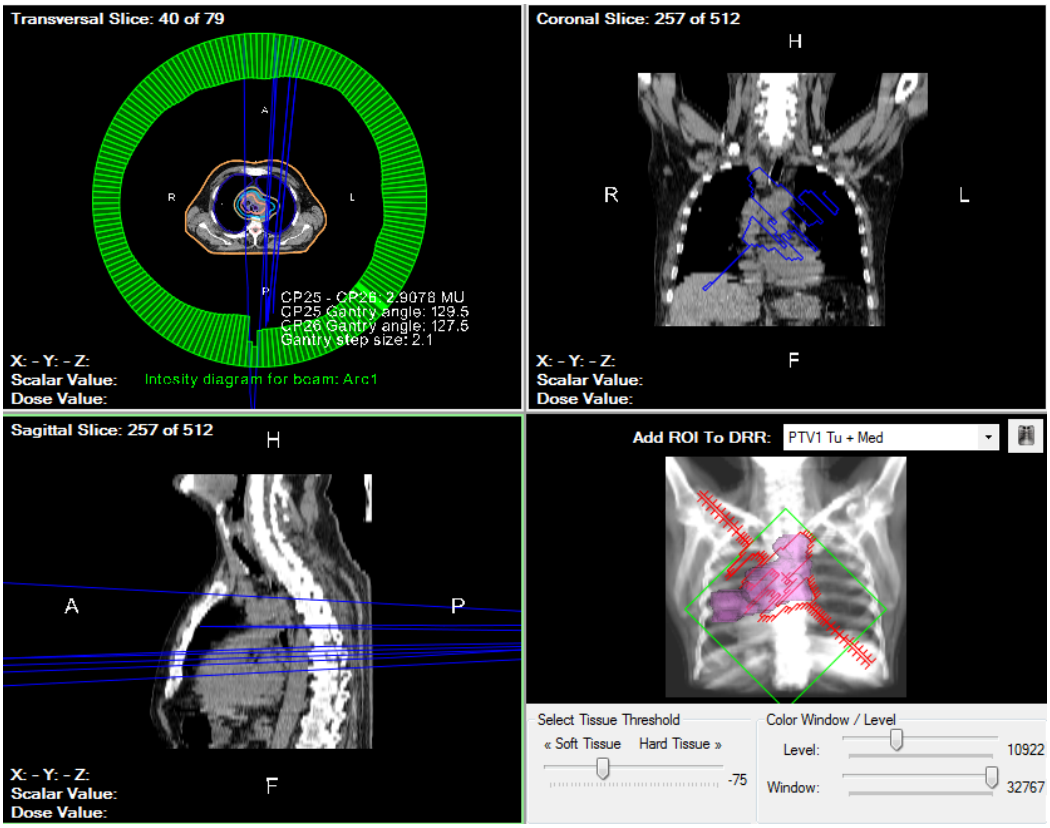

Figure 16 Dynamic arc with Beams-Eye-View

10.2.1 Beam Intensity Diagram

Beam Intensity Diagram can be displayed in transversal view. For dynamic arc plans, "Show Beam Intensity Diagram " option is enabled in Visible Beams window (Figure 14). When this option is checked, a diagram will be displayed, as shown in transversal view on Figure 16.

The height of the bins displays monitoring units (MUs) stored as a difference between two control points. Hovering with the mouse above the bins highlights the selected bin and displays the MUs, gantry angles for two control points and gantry step size in degrees.

In avoidance region, the MUs are equal to 0 for each control point. The corresponding diagram contains a red sector for all MU=0, as shown on Figure 17.

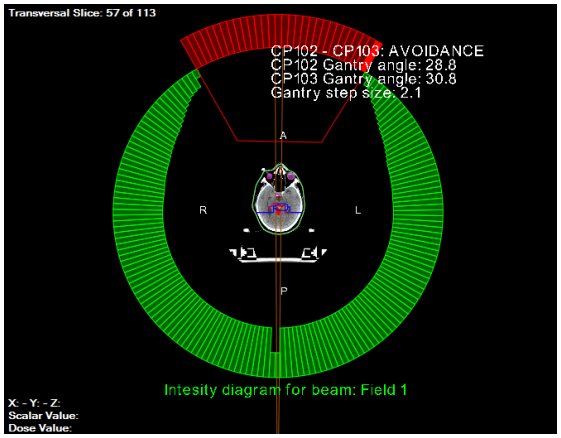
Transversal Slice: 57 of 113
CP102 - CP103: AVOIDANCE
CP102 Gantry angle: 28.8
CP103 Gantry angle: 30.8
Gantry step size: 2.1
Intesity diagram for beam: Field 1
X: - Y: - Z:
Scalar Value:
Dose Value:

Figure 17 Avoidance region of a RapidArc plan

10.2.2 Live Beams-Eye-View

You can switch the default volume rendering to live Beams-Eye-View - a live DRR generator for dynamic arc plans. Therefore, go to the menu 3D->Visible In 3D->Live Beams Eye View, or click on the Visible In 3D button on the toolbar (button 24 on Figure 8) and select Live Beams Eye View. Select a beam from Visible Beams window.

A DRR with projected vectorized collimator outlining will appear in the bottom right window, as shown on Figure 16. You can adjust the tissue threshold by setting the value with the slider towards soft or hard tissue, change level and window settings and add ROIs to DRR. By pressing the right mouse button and moving the cursor up and down you can zoom in and out. When looping through the list of beam control points, a new DRR will be automatically generated for each control point.

Live Beams-Eye-View feature generates DRRs using ray cast method. For performance reasons, DRRs are produced at lower quality of 133 by 133 points with spacing of 4,5 by 4,5 mm. By pressing on the DRR button in the upper right corner of the Live Beams-Eye-View window, you will obtain a high resolution DRR of 300 by 300 points with spacing of 2,0 by 2,0 mm.

11 Dose

Dose is visualized in 2D with lines and colorwash and as a wireframe in 3D (see Figure 18).

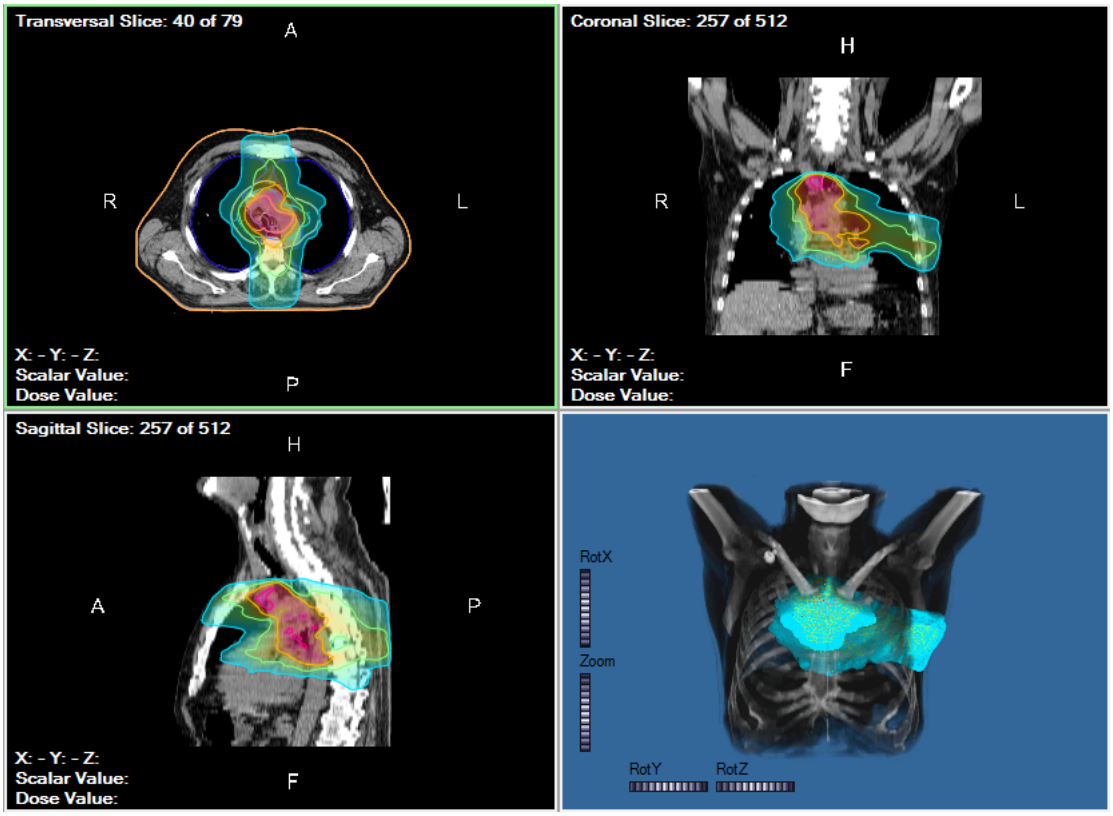

Figure 18 Dose lines and colorwash

To see absolute dose values, hover with the mouse above the image. Absolute dose values in Gy will be displayed at the bottom of the viewing window.

You can use the Cropping tool to cut through volume and dose and see internal dose distribution in 3D (see section “13 Cropping”).

11.1 Dose lines and colorwash

To visualize dose, go to All->Dose->Show Dose Lines, or click on the Show Dose drop-down button on the toolbar (button 5) and select Show Dose Lines. This will also turn on dose visualization in 3D.

To add dose colorwash visualization, go to All->Dose->Show Dose Colorwash, or click on the Show Dose drop-down button on the toolbar (button 5 on Figure 8) and select Show Dose Colorwash.

11.2 Visible Dose Values

You can adjust visible dose lines using Visible Dose Values screen. Go to All->Dose->Visible Dose Values, or click on the Show Dose drop-down button on the toolbar (button 5 on Figure 8) and select Visible Dose Values. In the Visible Dose Values window (see Figure 19) you can:

- Switch between absolute and normalized dose;
- Add/Edit/Remove points for color mapping;
- Add and Remove dose value;
- Select/unselect dose values for absolute dose and percentages for normalized dose.

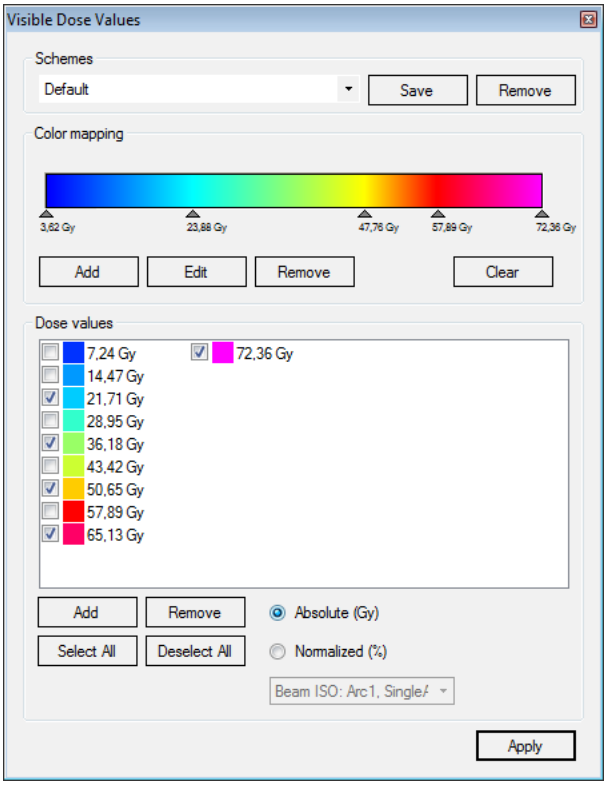

Figure 19 Visible Dose Values

When viewing normalized dose, you can select a normalization point which can be any of the POI's from the list.

To create a new scheme for visible dose values you can edit, remove or add values to the color legend. Depending on whether you create a scheme for absolute or normalized dose, the value you

have to provide when editing or adding a point is in Gy or percentage. Yu can also pick a color, as shown on Figure 20.

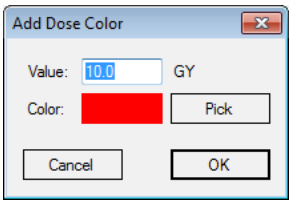

Figure 20 Add Dose Color

You can also create color schemes with negative dose values. These are used when presenting results of dose difference calculation of two plans in order to show which of two plans is better, as described in section 11.4.

From the defined color legend you can select specific values that you would like to display by checking the boxes next to the dose values, removing existing values and adding new ones.

You can save your color scheme under a new name.

11.3 Dose Volume Histogram (DVH)

To view DVH, go to All->Dose->Show Dose Volume Histogram, or click on the Show Dose drop-down button on the toolbar (button 5 on Figure 8) and select Show Dose Volume Histogram.

To calculate DVH:

- check one or more ROIs in the Active Plan tab for which you would like to calculate the DVH;
- optionally, if more than one plan is opened, select the plan to compare in the Compare tab, select the line type and the ROIs;
- check the option “Use calculated DVH” which is checked by default if no DVH is stored.
- when DVH calculation is completed, the Combined tab will contain the ROIs from the selected plans, together with DVH statistics.

For faster calculation, you can change the value of the Acceleration factor. By default the acceleration factor equals 1, which means that the algorithm will iterate through every dose voxel. Other values for acceleration factor are 2 and 3, which means that the algorithm will iterate through every second, resp. third voxel. The accuracy of the calculation is that lower, but you can get a impression of how DVH would look like much faster, especially for large ROIs. However, it is not recommended to use values of the acceleration factor other than 1 for smaller ROI.

You can switch between absolute and normalized values on the X-axis. Normalization can be done for any available POI that you can select from the drop-down box.

By hovering with the mouse above the DVH lines, you can see the exact values for absolute dose and volume. If you hover with the mouse above the grid lines in the Combined tab, the corresponding ROI will be highlighted on the graph.

Figure 21 shows an example DVH of two plans.

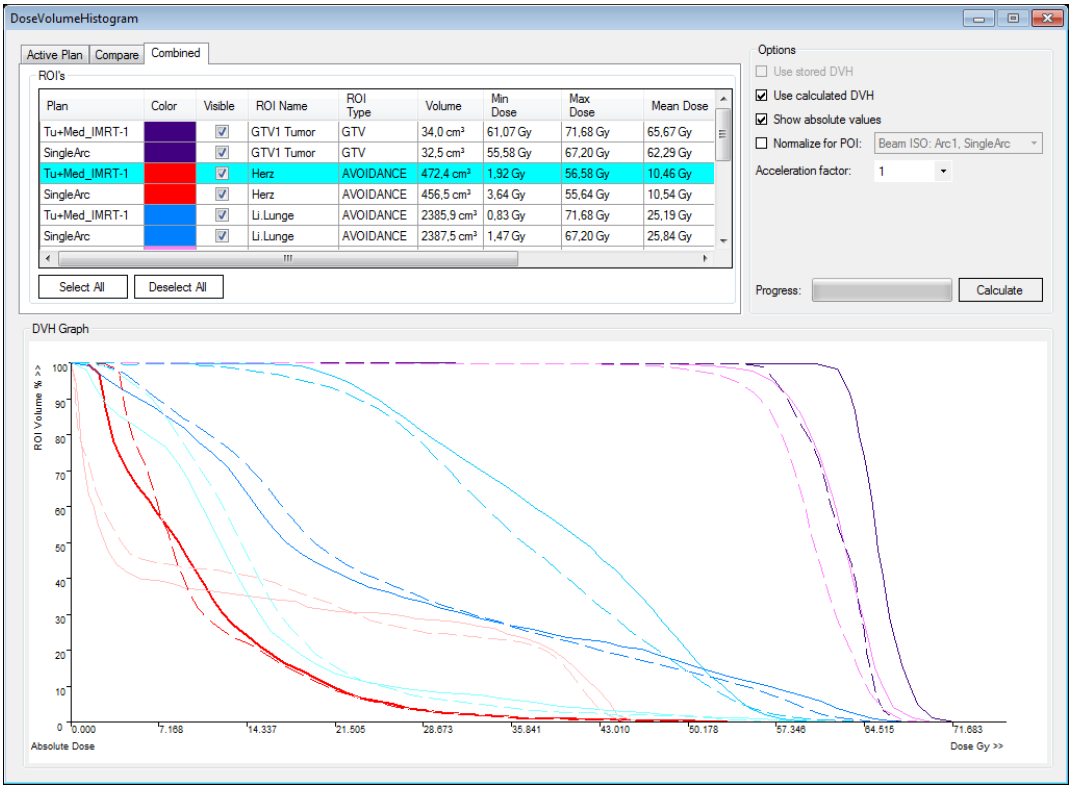

Figure 21 DVH

DVH calculation runs on a separate thread, so you can continue working with the application while the calculation takes place on the background. The calculated DVH is kept in the memory while the dataset is opened, so closing the DVH window and opening it again does not require recalculation of the DVH.

11.4 Dose Accumulation and Dose Difference

If the loaded dataset consists of 2 or more plans, the application can calculate dose accumulation and dose difference, provided that the plans reference the same set of CT scans.

Go to All->Dose->Dose Accumulation/Difference, or click on the Show Dose drop-down button on the toolbar (button 5 on Figure 8) and select Dose Accumulation/Difference. In the window, as shown on Figure 20, select two plans, select from which of these plans the application should take the ROIs and POIs for the new plan (if the original plans reference the same ROIs/POIs, then it does not matter which plan to check), and specify the calculation type - Accumulation or Difference.

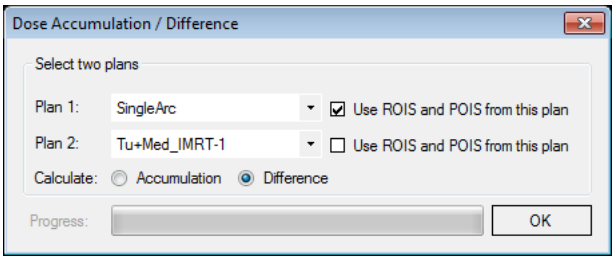

Figure 22 Dose Accumulation / Difference

For Dose Difference calculation the order of Plan 1 and Plan 2 is important, as the result will be displayed using negative and positive dose values to show which of two plans gives more/less dose.

The result of Dose Accumulation/Difference will be a new plan that will be added to the drop-down menu with plans. This plan will contain the calculated RT dose object, RT struct, and CT images, but no beams. All operations, such as DVH calculation or visualization of ROIs on coronal and sagittal slices, can be performed with the resulting plan.

Dose Accumulation/Difference can be applied for any number of plans recursively by specifying two plans at a time and then selecting another plan together with the newly created plan and running the calculation again.

11.5 Dose Objects

A study can contain several dose objects. By default, the application displays the total dose for the plan, but other dose objects can be selected if available.

Go to All->Dose->Dose Objects, or click on the Show Dose drop-down button on the toolbar (button 5 on Figure 8) and select Dose Objects. In the window, as shown on Figure 21, individual dose objects can be selected. If you select several objects, the displayed dose is the sum of these objects.

By default, the application shows the total plan dose (dose object PLAN). If this object is not present, it than searches for dose per beam objects (dose object BEAM) and displays the sum of these objects to get the total dose.

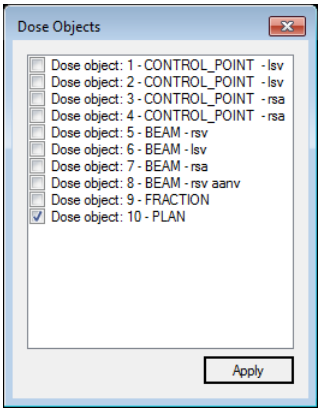
Dose Objects
Dose object: 1 - CONTROL_POINT - lsv
Dose object: 2 - CONTROL_POINT - lsv
Dose object: 3 - CONTROL_POINT - rsa
Dose object: 4 - CONTROL_POINT - rsa
Dose object: 5 - BEAM - rsv
Dose object: 6 - BEAM - lsv
Dose object: 7 - BEAM - rsa
Dose object: 8 - BEAM - rsv aanv
Dose object: 9 - FRACTION
Dose object: 10 - PLAN
Apply

Figure 23 Dose Objects

12 DRR

The DRR Viewer displays stored DRR images and allow you to generate DRRs per beam and beam control point. The vectorized collimator outlining will be projected on the image and can be switched on and off.

To open DRR viewer, go to All->DRR Viewer, or click on the DRR Viewer button on the toolbar (button 1 on Figure 8). You can use arrows on top of the viewer (buttons 1 and 2 on Figure 24) to scroll through stored DRR images and use Color Level and Color Window sliders to adjust Level and

Window values. When "Apply to all images" is checked, the application will apply the user-defined Level and Window values to all images shown in the DRR window.

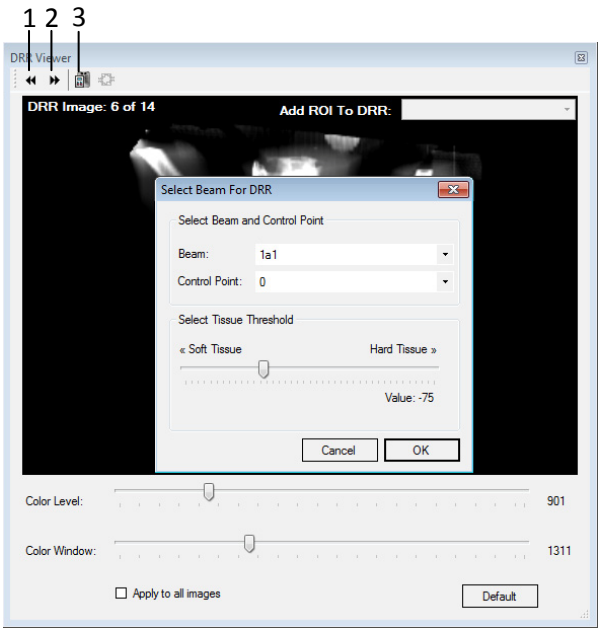

Figure 24 DRR beam selection

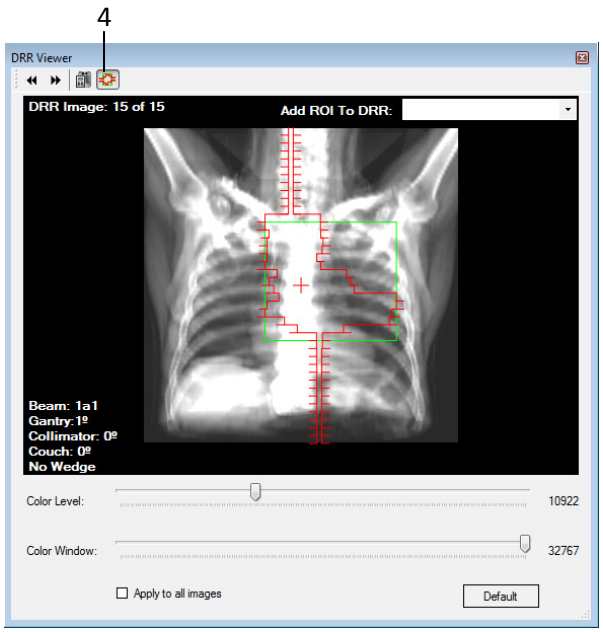

Figure 25 DRR with collimator outlines

To generate a DRR with vectorized collimator outlining, click on button 3 as shown on Figure 24. "Select Beam for DRR" window will appear where you can select a beam , beam control point if available, and set the tissue threshold towards soft or hard tissue for DRR calculation.

After the calculation has been completed, you will see the output as shown on Figure 25. You can turn the collimator outlining on and off using button 4 on Figure 25. You can also select ROI from the drop-down list that will be projected on the DRR.

The following operations for manipulation with the image are supported:

- Rotate image with the mouse by pressing Ctrl + left mouse button,
- Move image with the mouse by pressing Shift + left mouse button,
- Zoom in and out by pressing right mouse button and moving the mouse cursor up and down,
- Change window size.

The calculated DRR has a resolution of 300 by 300 points with spacing of 2,0 by 2,0 mm.

13 Distance measurement

You can measure distance between two points in transversal, coronal and sagittal views. Go to All->Measuring Tool, or click on the Measuring Tool button on the toolbar (button 12 on Figure 8). Then click on a starting point in the image and draw the measuring line to another point. The measured distance will be displayed on top of the viewing window (see Figure 26).

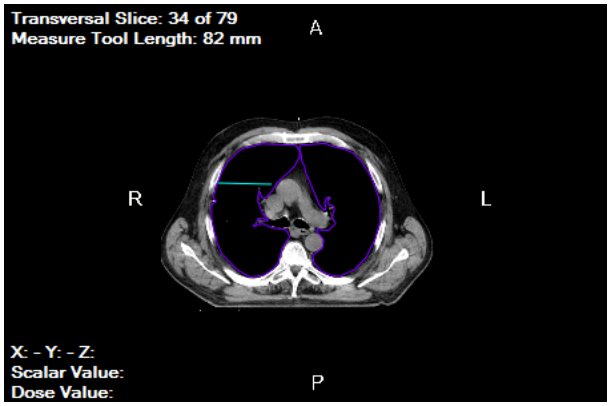

Figure 26 Measuring tool

14 Position Tracking

With Position Tracking tool, you can localize a point on any of 2D views and find the corresponding slices in other 2D views. In addition, you can trace the selected point in 3D.

To use Position Tracking, go to All->Position Tracking, orclick on the Position Tracking button on the toolbar (button 13 on Figure 8). A cross will appear on the active slice that will follow the mouse cursor, as shown on Figure 27.

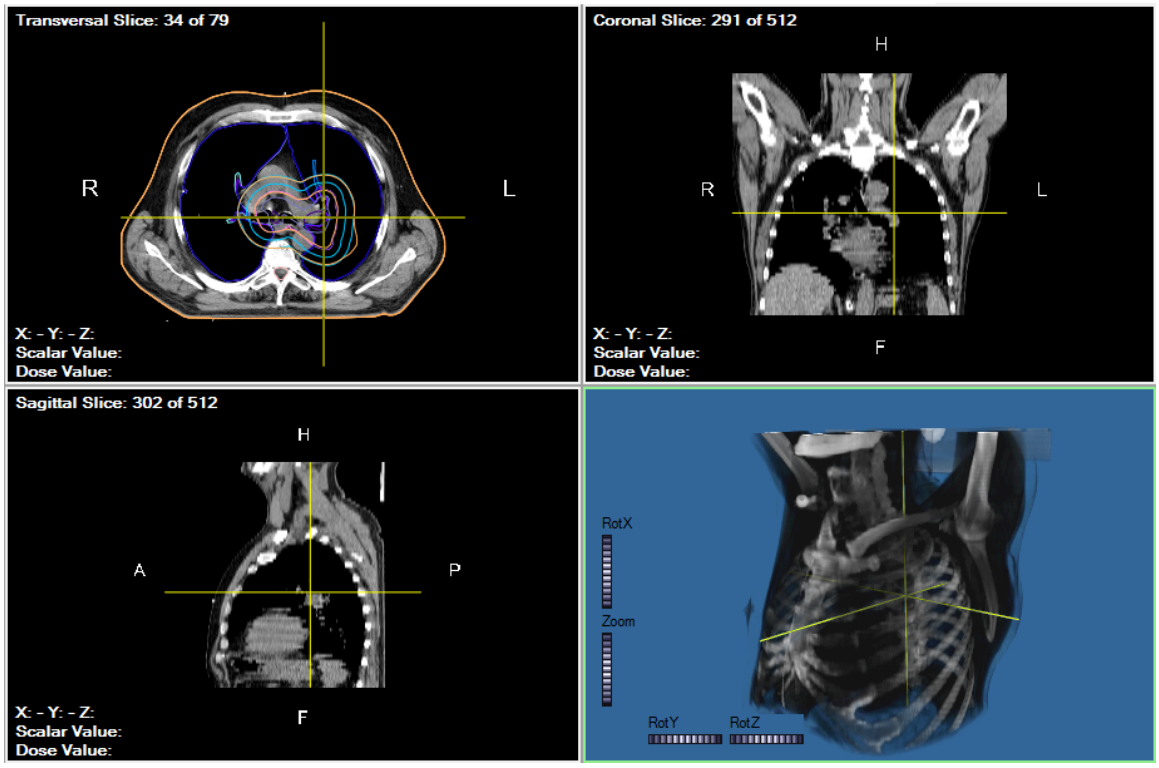

Figure 27 Position tracking in 2D and 3D

15 Cropping

The cropping tool allows slicing of volume and dose in 3D using 2D manipulators positioned in transversal, coronal and sagittal viewing windows.

To activate cropping, go to 2D->Cropping, or click on the Cropping button on the toolbar (button 20 on Figure 8). Cropping filters will be displayed in transversal, coronal and sagittal views, as shown on Figure 28.

Transversal cropping tool is a rectangle with grippers on each side and in the corners. Using the grippers, you can change the size of the rectangle. When hovering with the mouse above the edges of the rectangle, pan function will be activated and you can move the whole rectangle into a new position.

Coronal and sagittal cropping cuts the volume in height with two horizontal lines. The volume between the lines will be displayed. Changing cropping position in coronal view will automatically adjust it in sagittal view and vice versa.

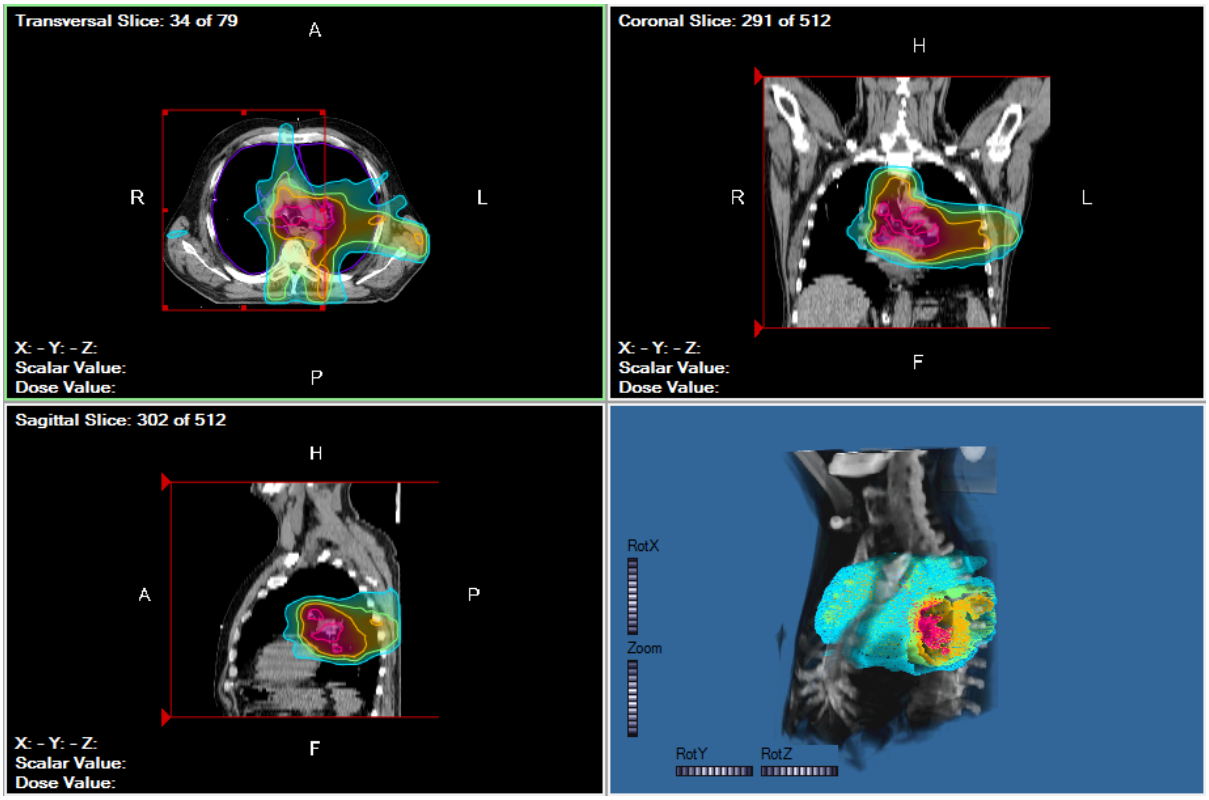

Figure 28 Cropping

16 Image Window / Level

To change Image Window / Level values, go to 2D->Image Window / Level, or click on the Image Window / Level button on the toolbar (button 21 on Figure 8).

The values can be adjusted using Color Level and Color Window sliders, also represented as red and blue vertical lines on the histogram (see Figure 29).

Normal and Cumulative histograms are supported.

Below the histogram there is a double ended slider to adjust the range of scalar values.

You can select predefined values for different organs from Profile drop-down menu. Alternatively, you can specify your own combination of Level and Window values and store them locally as a user-defined preset.

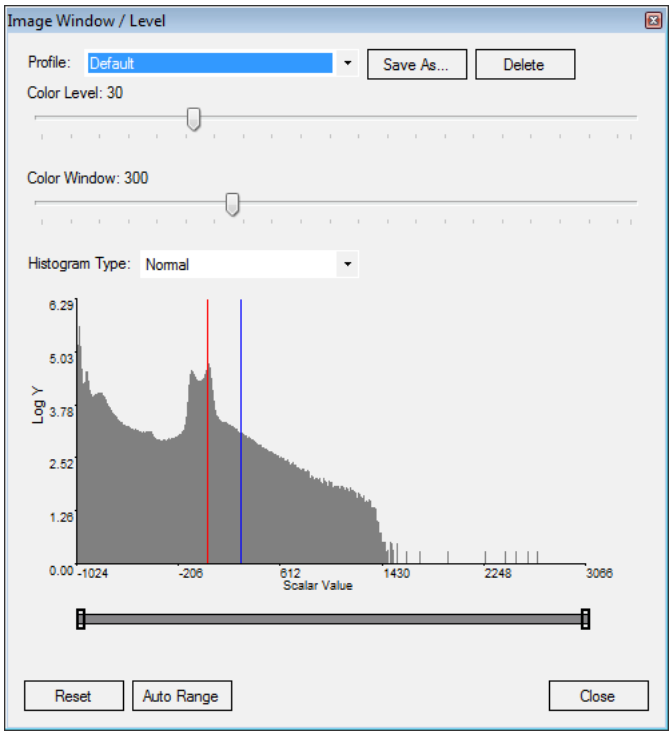

Figure 29 Image Window / Level

17 Magnifier

Magnifier allows you to zoom in on images details as if you were using a magnifying glass.

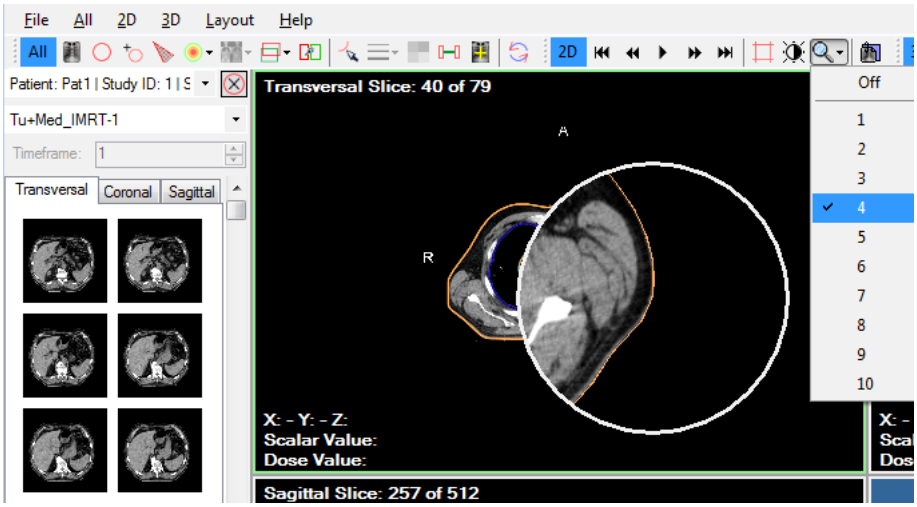

Figure 30 Magnifier

To switch on Magnifier, click inside the viewing window where you would like to use Magnifier. That will activate the window. Now go to 2D->Magnifier, or click on the Magnifier button on the toolbar (button 22 on Figure 8), and select zooming factor 1-10. Magnifier will appear in the active viewing window, as shown on Figure 30. Move the magnifier with the mouse while pressing left mouse button to view image details.

To turn off Magnifier, select “Off” from the Magnifier menu.

18 Reporting Tool

The Reporting Tool generates images from the transversal, coronal and sagittal views with projected beams, dose and structures in a grid layout and saves them as .png files.

To use the Reporting Tool, first define what you would like to see in the transversal, coronal and sagittal views by switching on/off beams, dose and structures. The images in the report will appear exactly as you define them in those views. Now go to 2D->Reporting Tool, or click on the Reporting Tool button on the toolbar (button 23 on Figure 8). The window, as shown on Figure 31, will appear.

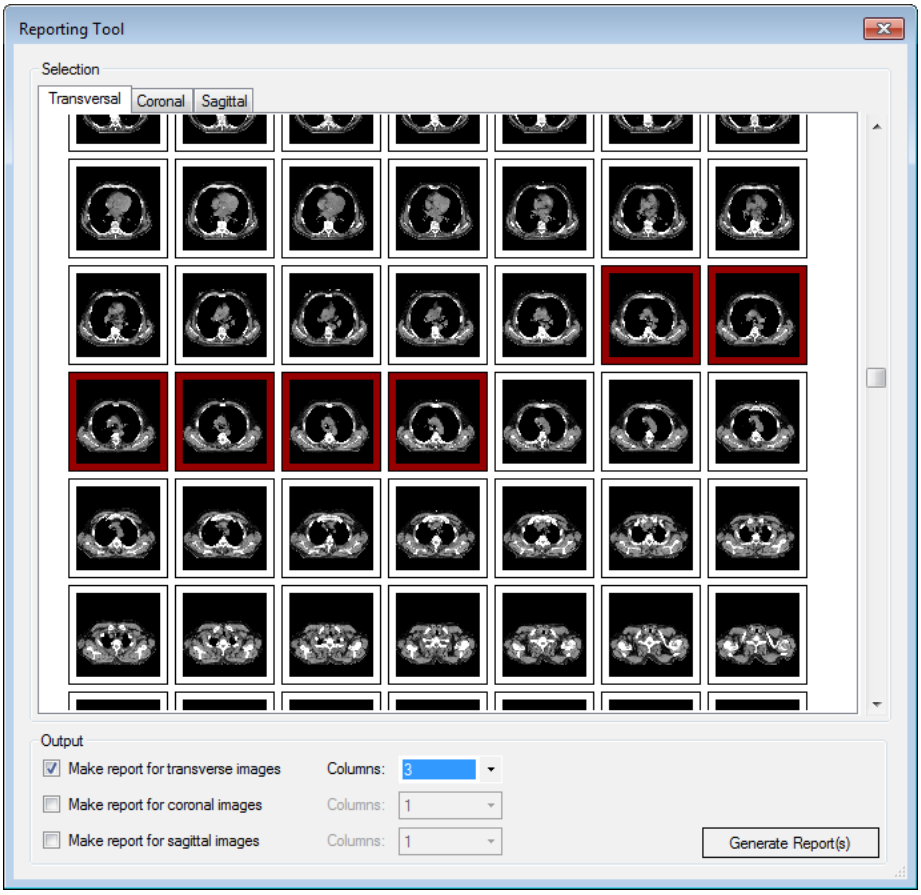

Figure 31 Reporting Tool image selection

The Reporting Tool window contains 3 tabs for transversal, coronal and sagittal thumbnailed images. Click on the thumbnails to select images you would like to include in your report. In the Output group check which image groups (transversal, coronal, sagittal) should be included and specify the number of columns per image group.

Figure 32 shows an example of a report with 6 transversal images in a 3 column layout.

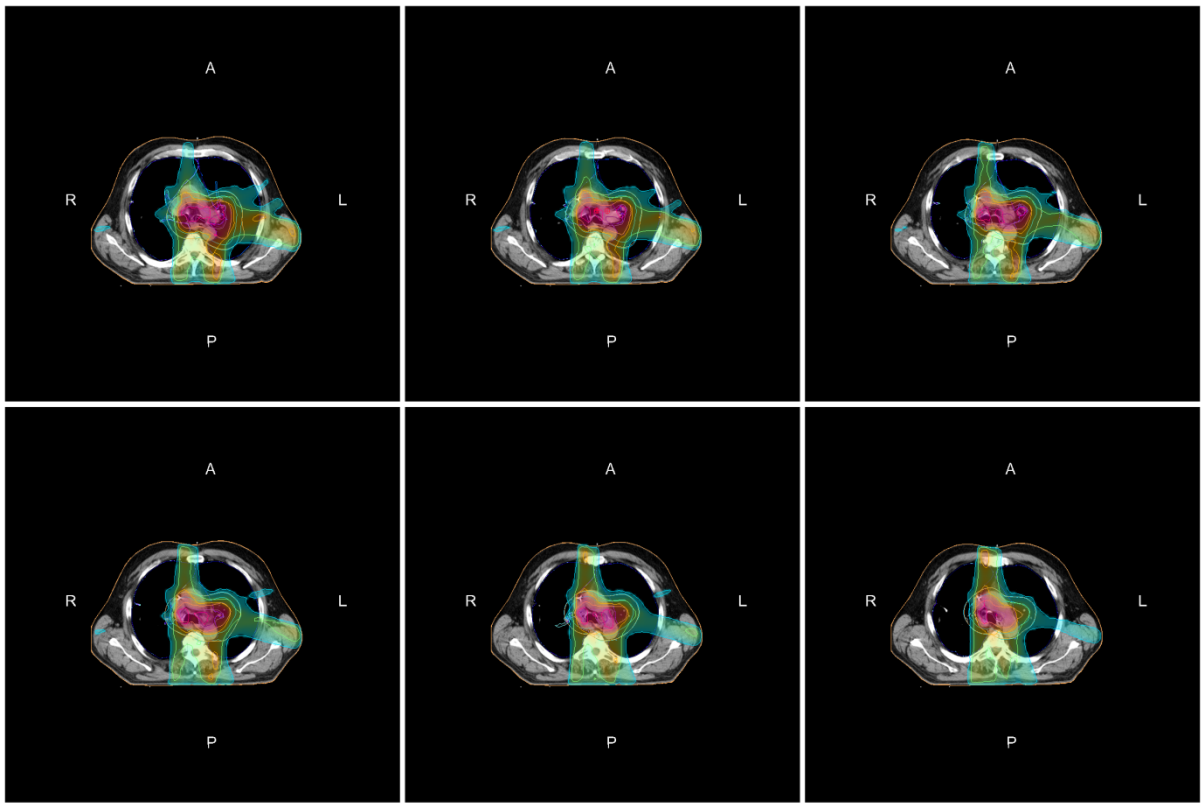

Figure 32 Reporting Tool output

19 3D viewing

19.1 Volume and Surface rendering

The 3D viewing component is capable of rendering the data as a semitransparent volume and surface. Volume rendering allows you to see internal organs similar to as they appear on X-ray images. Surface rendering extracts structures, such as skin and bone, and displays them as a surface.

You can switch between volume and surface rendering by going to 3D->Visible In 3D->Volume Rendering and Surface Rendering, or by clicking on the Visible in 3D drop-down button on the toolbar (button 24 on Figure 8).

Once in surface rendering mode, the Surface Rendering window will appear, where you can select a predefined type of surface rendering. You can also open this window by clicking on the Surface Rendering Options button on the toolbar (button 25 on Figure 8), or selecting it from the menu via 3D->Surface Rendering Options.

19.2 Skin with collimator outlining

Skin with collimator outlining is a particular type of surface rendering. If the viewer is in default volume rendering mode, you have to switch to surface rendering first. Therefore, go to 3D->Visible In 3D-> Surface Rendering, or click on the Visible in 3D drop-down button on the toolbar (button 24 on Figure 8) and select Surface Rendering.

In the Surface Rendering window select “CT- Skin + Collimator Outlining”, as shown on Figure 33. This will present a list of all beams. By clicking on the checkbox next to the beam name you can select/unselect the beam that will be projected on the skin as a contour (see example on Figure 34). If the beam has multiple control points, the Control Point drop-down box will be enabled, so you can select control point to use in the beam projection.

Additionally, for a better view, you can switch on beam geometry visualization in 3D by going to 3D->Visible In 3D, or clicking on Visible In 3D drop-down button on the toolbar (button 24 on Figure 8) and turning on Show Beams option.

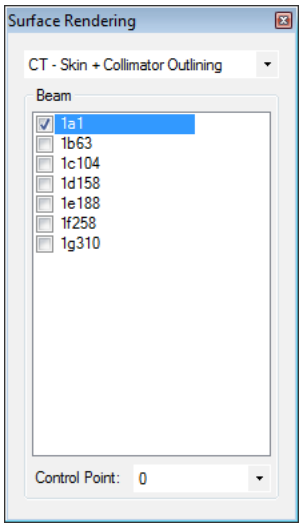

Figure 33 Skin Rendering window

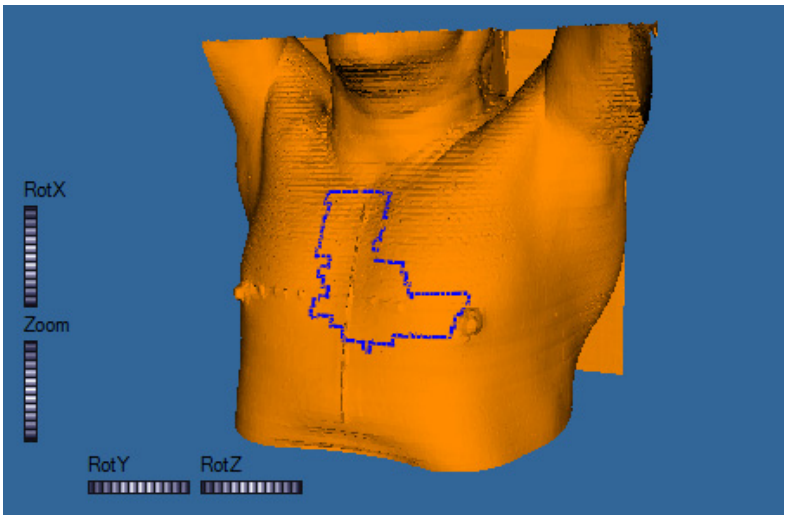

Figure 34 Skin Rendering with collimator outlines

19.3 3D settings

3D settings allow you to define volume view using opacity and color mapping. You can define your own filters and store them as presets, or use default filters.

3D rendering settings apply to volume rendering only! They are not intended and do not work for surface rendering!

To change 3D settings, go to 3D->3D Settings, or click on the 3D settings button on the toolbar (button 32 on Figure 8).

The 3D Rendering Settings window has 4 tabs: Opacity, Color, Presets and 4D Options.

The Opacity function allows you to define a filter for transparency by adding points and placing them in the histogram of grey values to create a transfer function, as shown on Figure 35.

The Color function works in a similar way by mapping color values to scalar values in a specified range (see Figure 36).

Both Opacity and Color functions work interactively in real time, which means that you will see the output in volume rendering as soon as you make an adjustment to your filter.

When PET-CT is rendered, 3D settings can be applied to either CT or PET volume using the drop-down menu at the top of the 3D Rendering Settings window (disabled for single volume).

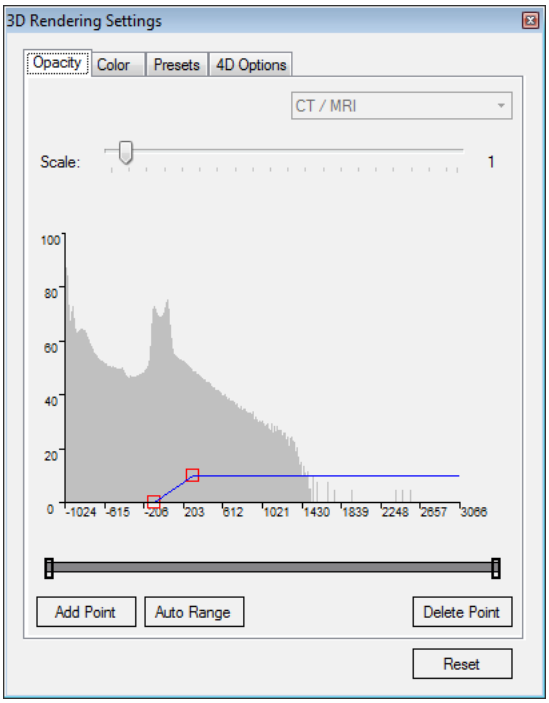

Figure 35 Volume Opacity

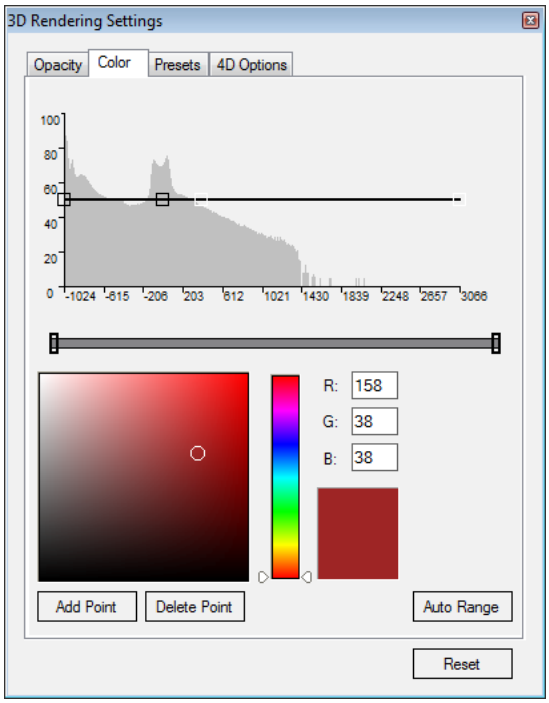

Figure 36 Volume Color

To save a filter, click on the Presets tab, then click on Save As button and enter a new name. Both opacity and color filter will be saved.

To load a filter, just select one from the drop-down menu in the Presets (see Figure 37).

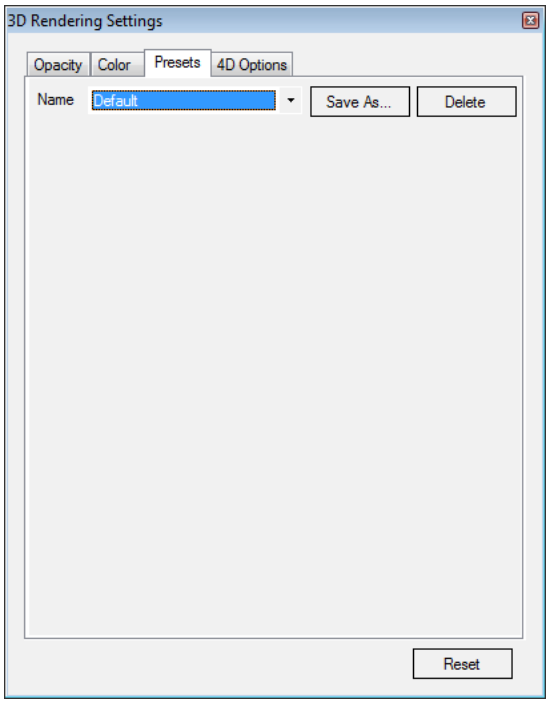

Figure 37 3D Presets

19.4 Shade

When using volume rendering, you can also add Shade in some cases for a more contrast view. However, shade will typically slow down the rendering and make interaction (rotation, zoom, pan) a bit slower.

To select/unselect shade, go to 3D->Shade, or click on the Shade button on the toolbar (button 33 on Figure 8).

19.5 3D slice positions

You can visualize positions of the active transversal, coronal and sagittal slices in 3D. Go to 3D->3D Slice Positions, or click on the 3D Slice Positions button on the toolbar (button 34 on Figure 8). In the 3D Slice Positions window check the slice positions you would like to see (see Figure 38). Slices will be shown as semitransparent planes that move as you scroll through the data in 2D viewing windows.

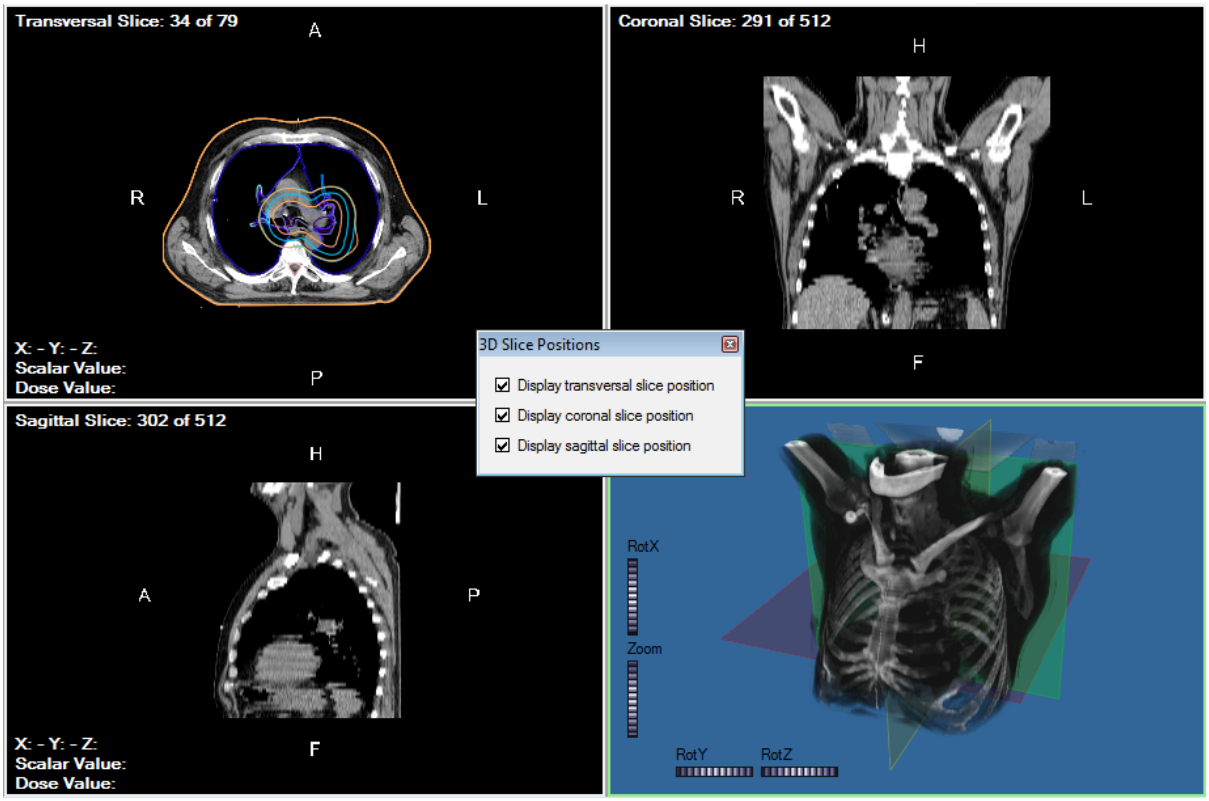

Figure 38 3D slice positions

20 PET-CT

PET-CT consists of two volumes that will be loaded together. To activate PET visualization on CT, go to All->PET, or click on the Show PET button on the toolbar (button 6 on Figure 8), and select a PET volume. There might be more than one PET available for the same set of CT scans.

To display PET in 3D, go to 3D->Visible In 3D->CT & PET, or click on the Visible In 3D drop-down button on the toolbar (button 24 on Figure 8), and select CT & PET. Please be aware that PET-CT

rendering in 3D requires substantial CPU resources to merge two volumes and will take time to calculate the final view!

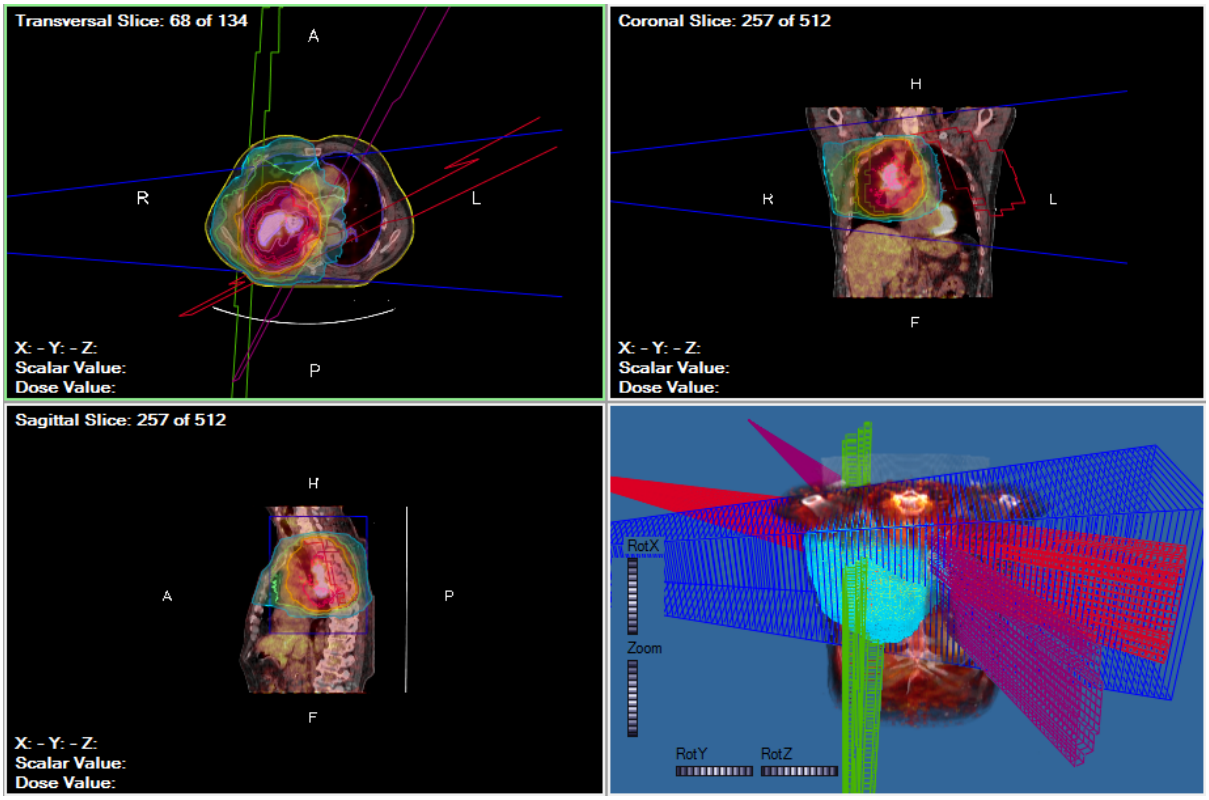

Figure 39 PET-CT with beams, ROIs and dose

When rotating PET-CT volume in 3D, the software will decrease the level of details while spinning and will recalculate the high quality presentation when spinning is stopped.

20.1 PET options

You can adjust PET color setting and PET position in PET Options window. Go to All->PET->PET Options, or click on the Show PET drop-down button on the toolbar (button 6 on Figure 8) and select PET Options.

You can chose from one of the widely use PET color schemes, adjust Level and Window settings, and specify transparency threshold (see Figure 40). Adjusting the Level and Window settings works similar to the Image Level/Window for CT images, allowing to display a selected range of PET values.

The application supports only pre-registered PET-CTs. If PET is not aligned properly with CT, you can adjust PET's position by specifying translation in X, Y and Z direction on the Move tab (see Figure 41). You can use both positive and negative numbers to specify direction of translation.

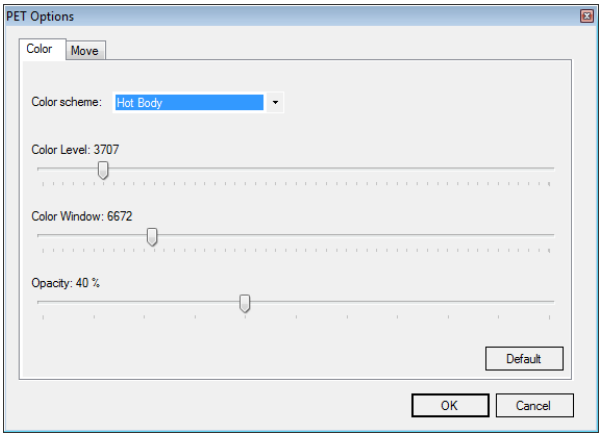

Figure 40 PET color/opacity

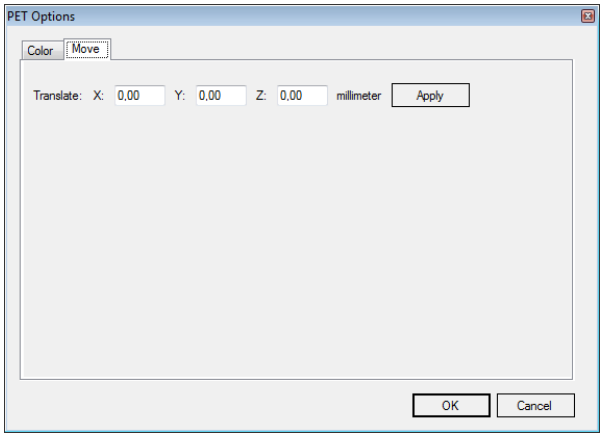

Figure 41 PET position

21 Viewing registered images

Registered images can be viewed using Overlay feature. The registration data should be stored in DICOM registration modality.

If multiple image sets are loaded, click on button 7 on Figure 8 to load an image set as a overlay. "Registration info loaded" will appear after the name of the dataset if registration data is available. The overlay image is visualized as chessboard, as shown on Figure 42.

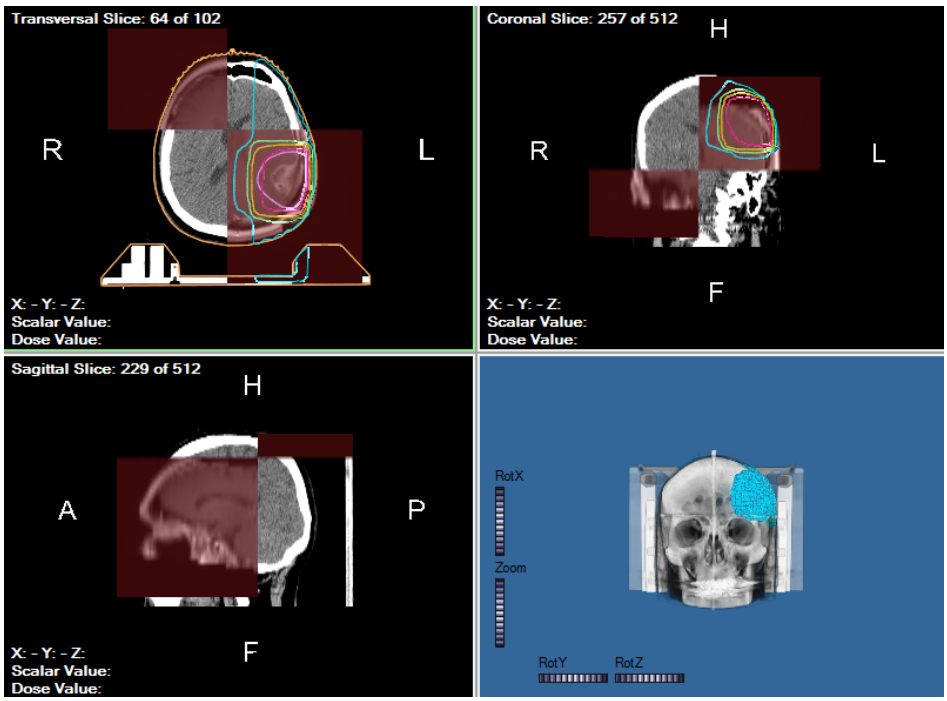

Figure 42 Overlay options

Using Overlay options, you can define the check size, opacity and select "Colored" option to view colored overlay. You can move the checks of the overlay over the image with the mouse while holding the left mouse button.

Figure 43 Overlay options

You can display ROIs/POIs, dose and beams, together with the overlay image.

22 Plan comparison

To compare two plans side by side, click on "Compare Plans" icon on the toolbar (button 8 on Figure 8). A window will appear where you can select two plans from the loaded plans and specify the view for comparison - transversal, coronal, or sagittal - as show on Figure 44.

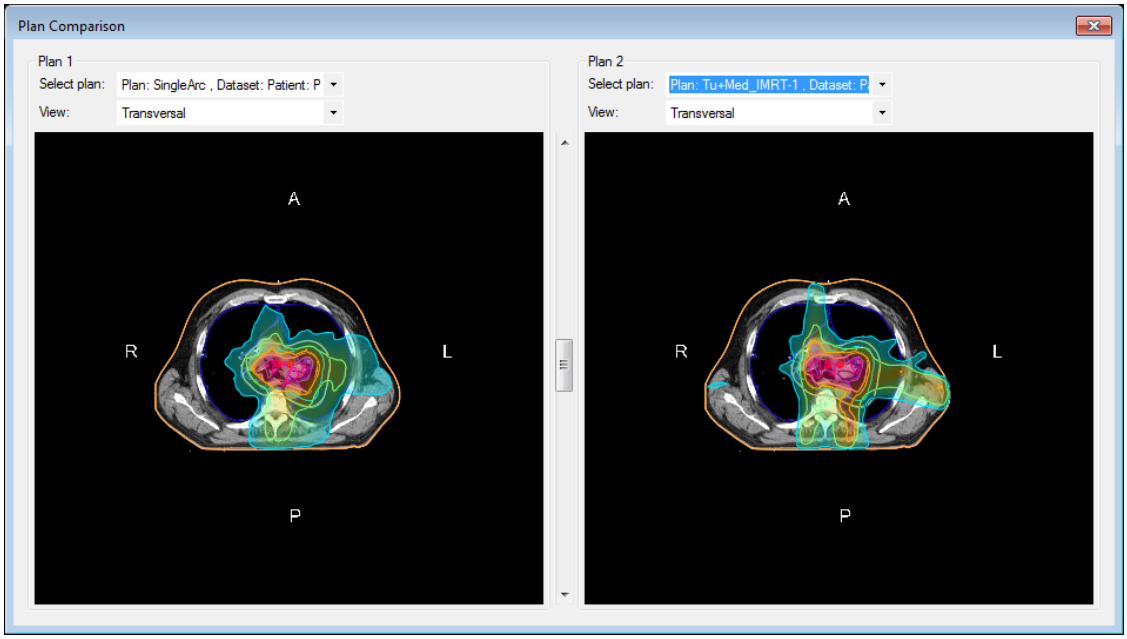

Figure 44 4D options

While Plan Comparison window is open, the toolbar and the main menu of the application are accessible. You can display ROIs/POIs, dose and beams in Plan Comparison window for each selected plan by using the tools from the main menu or the toolbar.

The dose lines and colorwash are turned on and off for both plans simultaneously when you use these features. The ROIs/POIs and the beams have to be turned on/off per plan. Therefore you have to active the plan first by selecting it from the drop-down plan menu 2 on Figure 7.

Plan comparison works on the same set of images.

23 4D

To load 4D datasets, see section “4.5 Loading 4D data”.

In 4D mode the application will enable the timeframe control (control 3 on Figure 7), so you can browse through frames per slice.

In 3D viewing window a 4D dataset will loop through frames, so you could see volume changes in time. You can adjust the refresh rate by going to 3D->3D Settings, or clicking on the 3D settings button on the toolbar (button 32 on Figure 8), and selecting 4D Options tab in the 3D Rendering Settings window. Set the frame speed in milliseconds and click on Apply (see Figure 45).

All 3D settings, such as opacity and color, can also be applied to 4D data.

Note that 4D datasets are typically very large. So it might be the case that your machine will not have enough memory for a 4D dataset!

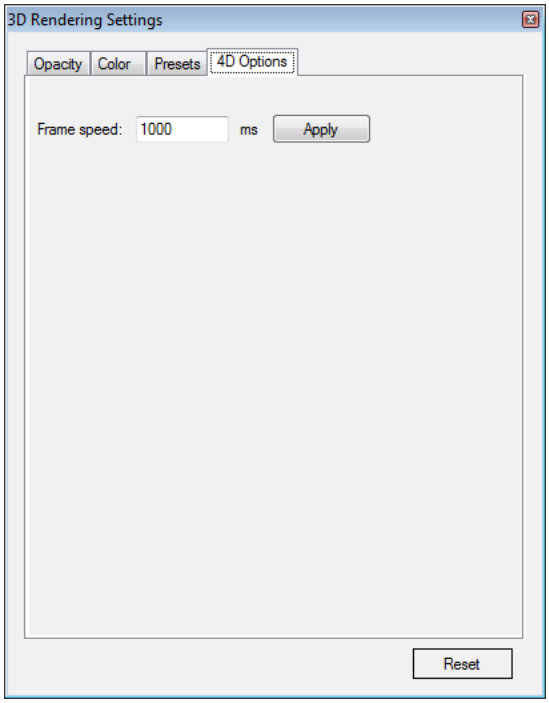

Figure 45 4D options